

Db 245 DMWSLGVIMYILLCGYPPFYFNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRN 304

QY 301 LLKTEPTQRMITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 360
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Db 305 LLKTEPTQRMITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 364
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QY 361 VDYEQIKIKKIEDASNPLLLKRRKKARALEAAALAH 396
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Db 365 VDYEQIKIKKIEDASNPLLLKRRKKARALEAAALAH 400
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RESULT 2
US-09-142-551A-3
; Sequence 3, Application US/09142551A
; Patent No. 6218136
; GENERAL INFORMATION:
; APPLICANT: KUMAR, SANJAY
; APPLICANT: LIVI, GEORGE P.
; APPLICANT: MCLAUGHLIN, MEGAN M.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: METHODS OF THE IDENTIFICATION OF
; TITLE OF INVENTION: PHARMACEUTICALLY ACTIVE COMPOUNDS
; FILE REFERENCE: P50448
; CURRENT APPLICATION NUMBER: US/09/142,551A
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US97/04256
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,286
; PRIOR FILING DATE: 1996-03-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-142-551A-3

Query Match 98.6%; Score 2076; DB 2; Length 396;
Best Local Similarity 99.0%; Pred. No. 3.7e-157;
Matches 392; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SQGQSPVPFPAPAPPQPTPALPHPPAQQPPPPQFPQFHVKSGLQIKKNAIIDDYK 60
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Db 1 SQGQSPVPFPAPAPPQPTPALPHPPAQQPPPPQFPQFHVKSGLQIKKNAIIDDYK 60
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QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPDIVRVDVY 120
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Db 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPDIVRVDVY 120
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QY 121 ENLYAGRKCLLI VMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 180
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Db 121 ENLYAGRKCLLI VMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 180
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QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYVVAPEVLGPEKYDKSC 240
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Db 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYVVAPEVLGPEKYDKSC 240
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QY 241 DMWSLGVIMYILLCGYPPFYFNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRN 300
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Db 241 DMLVLGVIMYILLCGYPPFYFNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRN 300
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QY 301 LLKTEPTQRMITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 360
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Db 301 LLKTEPTQRMITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 360
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QY 361 VDYEQIKIKKIEDASNPLLLKRRKKARALEAAALAH 396
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Db 361 VDYEQIKIKKIEDASNPLLLKRRKKARALEAAALAH 396
|||||

RESULT 3
US-09-142-551A-4
; Sequence 4, Application US/09142551A

; Patent No. 6218136
; GENERAL INFORMATION:
; APPLICANT: KUMAR, SANJAY
; APPLICANT: LIVI, GEORGE P.
; APPLICANT: MCLAUGHLIN, MEGAN M.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: METHODS OF THE IDENTIFICATION OF
; TITLE OF INVENTION: PHARMACEUTICALLY ACTIVE COMPOUNDS
; FILE REFERENCE: P50448
; CURRENT APPLICATION NUMBER: US/09/142,551A
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US97/04256
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,286
; PRIOR FILING DATE: 1996-03-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-142-551A-4

Query Match 88.0%; Score 1854; DB 2; Length 370;
Best Local Similarity 99.1%; Pred. No. 1.6e-139;
Matches 346; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SQGQSPVPFPAPAPPQPTPALPHPPAQQPPPPQFPQFHVKSGLQIKKNAIIDDYK 60
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Db 5 SQGQSPVPFPAPAPPQPTPALPHPPAQQPPPPQFPQFHVKSGLQIKKNAIIDDYK 64
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QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120
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Db 65 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPDIVRVDVY 124
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QY 121 ENLYAGRKCLLI VMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 180
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QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYVVAPEVLGPEKYDKSC 240
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Db 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYVVAPEVLGPEKYDKSC 244
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QY 241 DMWSLGVIMYILLCGYPPFYFNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRN 300
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Db 245 DMLVLGVIMYILLCGYPPFYFNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRN 304
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QY 301 LLKTEPTQRMITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 349
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Db 305 LLKTEPTQRMITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 353
|||||

RESULT 4
US-09-142-551A-2
; Sequence 2, Application US/09142551A
; Patent No. 6218136
; GENERAL INFORMATION:
; APPLICANT: KUMAR, SANJAY
; APPLICANT: LIVI, GEORGE P.
; APPLICANT: MCLAUGHLIN, MEGAN M.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: METHODS OF THE IDENTIFICATION OF
; TITLE OF INVENTION: PHARMACEUTICALLY ACTIVE COMPOUNDS
; FILE REFERENCE: P50448
; CURRENT APPLICATION NUMBER: US/09/142,551A
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US97/04256
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,286
; PRIOR FILING DATE: 1996-03-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2


```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 790790
;
US-08-878-989-19

Query Match 24.3%; Score 512.5; DB 1; Length 370;
Best Local Similarity 36.4%; Pred. No. 8.8e-33;
Matches 117; Conservative 68; Mismatches 95; Indels 41; Gaps 12;

QY 56 IDDYKVTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVE-----L 103
Db 19 IYDFR---DVLGTGAFSEVILAEDKRTQKLVAIKCI-----AKEALEGKEGSMENEIAVL 70

QY 104 HWRASQCPIHVRIVDVYENLYAGRKCLLIIVMECLDGGELFSRIQDRGDQAFTEREASEIM 163
Db 71 H--KIKHPNIVALDDIYES--GGH--LYLIMQLVSGGELFDRIVEKG--FYTERDASRLI 122

QY 164 KSIGEAIQYLHSINIAHRDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTP 223
Db 123 FQVLDAVKYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTP 182

QY 224 YVVAPEVLGPYKDYKSCDMWSLGVIMYILLCGYPPFYNSHGLAISPGMKTRIRMGQYEF 283
Db 183 GYVAPEVLAQKPYSKAVDCWSIGVIAVILLCGYPPFYDENDAKLF-----EQILKAEYEF 238

QY 284 NPEWSEVSEEVKMLIRNLKTEPTQRTMTITEFMNHPWIMQSTKVPQTPLH--TSRVLKED 341
Db 239 SPYWDIDSDSAKDFIRHLMKEKDPEKRFCEQALQHPWIAGDTALDKN-IHQSVSEIQIKN 297

QY 342 --KERWEDVKEEMTSALATMR 360
Db 298 FAKSKW----KQAFNATAVVR 314

RESULT 10
US-09-272-796-19
; Sequence 19, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
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; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 790790
;
US-09-272-796-19

Query Match 24.3%; Score 512.5; DB 2; Length 370;
Best Local Similarity 36.4%; Pred. No. 8.8e-33;
Matches 117; Conservative 68; Mismatches 95; Indels 41; Gaps 12;

QY 56 IDDYKVTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVE-----L 103
Db 19 IYDFR---DVLGTGAFSEVILAEDKRTQKLVAIKCI-----AKEALEGKEGSMENEIAVL 70

QY 104 HWRASQCPIHVRIVDVYENLYAGRKCLLIIVMECLDGGELFSRIQDRGDQAFTEREASEIM 163
Db 71 H--KIKHPNIVALDDIYES--GGH--LYLIMQLVSGGELFDRIVEKG--FYTERDASRLI 122

QY 164 KSIGEAIQYLHSINIAHRDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTP 223
Db 123 FQVLDAVKYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTP 182

QY 224 YVVAPEVLGPYKDYKSCDMWSLGVIMYILLCGYPPFYNSHGLAISPGMKTRIRMGQYEF 283
Db 183 GYVAPEVLAQKPYSKAVDCWSIGVIAVILLCGYPPFYDENDAKLF-----EQILKAEYEF 238

QY 284 NPEWSEVSEEVKMLIRNLKTEPTQRTMTITEFMNHPWIMQSTKVPQTPLH--TSRVLKED 341
Db 239 SPYWDIDSDSAKDFIRHLMKEKDPEKRFCEQALQHPWIAGDTALDKN-IHQSVSEIQIKN 297

QY 342 --KERWEDVKEEMTSALATMR 360
Db 298 FAKSKW----KQAFNATAVVR 314

RESULT 11
US-09-457-040B-31
; Sequence 31, Application US/09457040B
; Patent No. 6387641
; GENERAL INFORMATION:
; APPLICANT: Vertex Pharmaceuticals Incorporated
; APPLICANT: Bellon, Steve
; TITLE OF INVENTION: Crystallized P38 Complexes
; FILE REFERENCE: VPI/98-14
; CURRENT APPLICATION NUMBER: US/09/457,040B
; CURRENT FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 41
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 19, 2006, 14:43:31 ; Search time 7472 Seconds
(without alignments)
5083.615 Million cell updates/sec

Title: US-10-469-221-2
Perfect score: 2106
Sequence: 1 SQGQSPVPFPAPAPPPQPP.....PLLLKRRKKARALEAAALAH 396

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abses/ABSSWEB_spool/US10469221/runat_19062006_062550_1024/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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13: gb_in:*
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15: gb_da:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2106	100.0	1690	5 BC036060	BC036060 Homo sapi
2	2106	100.0	2974	5 BC052584	BC052584 Homo sapi
3	2078	98.7	1336	2 AR380852	AR380852 Sequence

4	2078	98.7	1336	5 HSMAPKAP	X75346 H.sapiens m
5	1991.5	94.6	2258	2 AR270852	AR270852 Sequence
6	1991.5	94.6	2258	2 AX335055	AX335055 Sequence
7	1991.5	94.6	2258	5 HSU12779	U12779 Human MAP k
8	1931	91.7	2586	6 BC063064	BC063064 Mus muscu
9	1930	91.6	2862	6 BC062048	BC062048 Rattus no
10	1930	91.6	2909	6 AY197741	AY197741 Rattus no
11	1927	91.5	2604	6 BC052206	BC052206 Mus muscu
12	1921	91.2	1247	6 MMAPKAP	X76850 M. musculus
13	1764	83.8	1065	8 AY335730	AY335730 Synthetic
14	1729	82.1	1305	2 DD182194	DD182194 Methods a
15	1709	81.1	1168	2 CS214061	CS214061 Sequence
16	1709	81.1	1168	6 CLMAPKAP	X82220 C.longicaud
17	1689	80.2	2977	11 BC070986	BC070986 Xenopus l
18	1672	79.4	2786	11 CR761979	CR761979 Xenopus t
19	1663.5	79.0	2503	11 BC084300	BC084300 Xenopus l
20	1645	78.1	3265	11 BC054572	BC054572 Danio rer
21	1391	66.0	1149	8 AY335561	AY335561 Synthetic
22	1391	66.0	1149	8 AY892450	AY892450 Synthetic
23	1391	66.0	1149	8 AY892451	AY892451 Synthetic
24	1391	66.0	1149	8 BT008118	BT008118 Synthetic
25	1391	66.0	1298	5 HSU43784	U43784 Human mitog
26	1391	66.0	2481	2 AR270525	AR270525 Sequence
27	1391	66.0	2481	5 HSU09578	U09578 Homo sapien
28	1391	66.0	2494	5 BC007591	BC007591 Homo sapi
29	1391	66.0	2519	5 BC001662	BC001662 Homo sapi
30	1391	66.0	2523	5 BC010407	BC010407 Homo sapi
31	1377.5	65.4	2654	14 BC103321	BC103321 Bos tauru
32	1371	65.1	2634	6 BC081974	BC081974 Rattus no
33	1365	64.8	2484	2 CQ716382	CQ716382 Sequence
34	1361	64.6	2856	6 BC031467	BC031467 Mus muscu
35	1347	64.0	768	14 OCMAPKAP	X75345 O.cuniculus
36	1333	63.3	1333	2 AR145880	AR145880 Sequence
37	1266	60.1	1544	13 DQ307182	DQ307182 Glossina
38	1243.5	59.0	2049	13 D82877	D82877 Hemientrot
39	1201	57.0	1982	13 DMU20757	U20757 Drosophila
40	1201	57.0	2000	2 CQ577905	CQ577905 Sequence
41	1201	57.0	2025	2 CQ601278	CQ601278 Sequence
42	1105	52.5	3949	13 AY069813	AY069813 Drosophil
43	1043	49.5	6276	2 CQ577904	CQ577904 Sequence
44	1043	49.5	6276	2 CQ601277	CQ601277 Sequence
45	1043	49.5	50394	12 AC014393	AC014393 Drosophil

ALIGNMENTS

RESULT 1	BC036060	1690 bp	mrna	linear	PRI 28-JUL-2005
LOCUS	BC036060	Homo sapiens mitogen-activated protein kinase-activated protein kinase 2, transcript variant 2, mRNA (cdna clone MGC:33670 IMAGE:5296259), complete cds.			
DEFINITION	BC036060	Homo sapiens (human)			
ACCESSION	BC036060	GI:23271276			
VERSION	BC036060.1	MGC.			
KEYWORDS	BC036060	Homo sapiens (human)			
SOURCE	BC036060	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
ORGANISM	BC036060	1 (bases 1 to 1690)			
REFERENCE	BC036060	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Loquellano,N.A., Peters,G.J., Carninci,P., Prange,C., Raha,S.S., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,			

Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y., Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smailus, D. E., Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A. Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1690)
NIH MGC Project
Direct Submission
Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 48 Row: 1 Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 32481207.
Location/Qualifiers

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:33670 IMAGE:5296259"
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/lab_host="DH10B"
/note="Vector: pBluescriptR"
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/gene="MAPKAPK2"
/db_xref="GeneID:9261"
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211. .1413
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protein kinase 2, isoform 2"
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/db_xref="GI:37590438"
/db_xref="GeneID:9261"
/db_xref="MIM:602006"
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QFVKSGLQIKNAIIDDYKVTSQLGLINGKVLOIFNKRTOEFALKMLQDCPKAR
REVELHWRASQCPIHIVDVYENLYAGRKCLLI VMECLDGGELFSRIODRGDQAFTE
REASEIMKSIGEAIQYLHSINIAHRDVKPENLLYTSKRPNAILKLTDFGFAKETTSN
SLTTPCYTPYVAPEVLGPEKYDKSCDMWSLGVIMYILLCGYPPFYSNHGLAISPGMK
TRIRMGQYFPNPEWSEVSEEVKMLIRNLLKTEPTQRTMTTEFMNHPWIMQSTKVPQT
PLHTRVLKEDKERWEDVKEEMTSALATMRVDYEQIKIKKIEDASNPLLLRKKKARA
LEAAALAH"

ORIGIN

Alignment Scores: 1.31e-178 Length: 1690
Pred. No.: 2106.00 Matches: 396
Score: 100.0% Conservative: 0
Percent Similarity:

Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0
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Db	223	TCCACGGGCCAGAGCCCGCGGTGCGTTC	282
QY	21	ThrProAlaLeuProHisProAlaGlnProProProProGlnGlnPhePro	40
Db	283	ACCCCTGCCCTGCCGACCCCGCGCGCAGCCCGCGCGCGCAGCAGTTCCCG	342
QY	41	GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleAspTyrLys	60
Db	343	CAGTTCACGTC AAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG	402
QY	61	ValThrSerGlnValLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys	80
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QY	81	ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu	100
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QY	101	ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr	120
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QY	161	GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis	180
Db	703	GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT	762
QY	181	ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys	200
Db	763	CGGGATGTCAAGCCTGAGAATCTCTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA	822
QY	201	LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys	220
Db	823	CTCACTGACTTTGGCTTGGCCAAAGGAAACCCAGCCCAACTCTTTGACCACCTCCTTGT	882
QY	221	TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys	240
Db	883	TATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAAGTATGACAAAGTCTCTGT	942
QY	241	AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProPropheTyr	260
Db	943	GACATGTGTCCCTGGGTGTCATCATGTACATCCTGTGTGGGTATCCCCCTTCTAC	1002
QY	261	SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr	280
Db	1003	TCCAACCAACCGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT	1062
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Db	1063	GAATTTCCCAACCCAGAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT	1122
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QY	321	IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu	340
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QY 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
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RESULT 2
BC052584
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DEFINITION
Homo sapiens mitogen-activated protein kinase-activated protein
kinase 2, transcript variant 2, mRNA (cdna clone MGC:59706
IMAGE:6267183), complete cds.
ACCESSION
BC052584
VERSION
BC052584.1 GI:30851682
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 2974)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932

REFERENCE
PUBMED
2 (bases 1 to 2974)
Strausberg,R.
Direct Submission
Submitted (16-MAY-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 47 Row: h Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 14589905.

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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

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Db 266 ACCCTGCGCTGCCGACCCCGCGCGAGCCGCGCGCCCGCAGCAGTTCCTCCG 325

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QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
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QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120

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Db 1046 GAATTTCCCAACCCAGAAATGGTCAGAAATATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1105

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Db 1106 CTGCTGAAAACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 1165

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Db 1286 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAAACCTCTGTGCTG 1345

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RESULT 3

AR380852

LOCUS AR380852 1336 bp DNA linear PAT 18-DEC-2003

DEFINITION Sequence 1397 from patent US 6607879.

ACCESSION AR380852

VERSION AR380852.1 GI:40088486

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1336)

AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.

TITLE Compositions for the detection of blood cell and immunological response gene expression

JOURNAL Patent: US 6607879-A 1397 19-AUG-2003;

Incyte Corporation; Palo Alto, CA

FEATURES

source 1. .1336

/organism="unknown"

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ORIGIN

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Score: 2078.00

Percent Similarity: 99.2% Conservative: 0

Best Local Similarity: 99.2% Mismatches: 3

Query Match: 98.7% Indels: 0

DB: 2 Gaps: 0

US-10-469-221-2 (1-396) x AR380852 (1-1336)

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QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspAspTyrLys 60

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QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160

Db 421 GAACTCTTTAGCCGAATCCAGGATCCAGGAGACCAGGCATTCACAGAAAGAGAAAGCATCC 480

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RESULT 4
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DEFINITION H.sapiens mRNA for MAP kinase activated protein kinase.
ACCESSION X75346
VERSION X75346.1 GI:407074
KEYWORDS MAP kinase activated protein kinase-2; protein kinase.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1336)
Stokoe,D., Caudwell,B., Cohen,P.T. and Cohen,P.
The substrate specificity and structure of mitogen-activated
protein (MAP) kinase-activated protein kinase-2
Biochem. J. 296 (Pt 3), 843-849 (1993)
8280084
2 (bases 1 to 1336)
Stokoe,D.H.
Direct Submission
Submitted (30-SEP-1993) D.H. Stokoe, MRC Protein Phosphorylation
Unit, Dept of Biochemistry, Medical Sciences Institute, The
University of Dundee, Dundee DD1 4HN, United Kingdom
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/dev_stage="adult"
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ORIGIN ALAH"
Alignment Scores: 3.18e-176 Length: 1336
Pred. No.: 2078.00 Matches: 393
Score: 99.2% Conservative: 0
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Best Local Similarity: 99.2% Indels: 0
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DB: 5
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Db 541 CGGGATGTCAAGCCTGAGAATCTTTATACACCTCCAAAAGGCCCAACGCCCATCTCTGAAA 600
QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
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QY 221 TyrThrProTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
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QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
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QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 841 GAAITTTCCCAACCCAGAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900

Db 1771 GCCAGGCTCTCTGTGCTGCCAGCGCTGGGGTGAGGCTGCGGTTGTAGCGTGGACCACTAA 1830

QY 349 ----- 349

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QY 349 ----- 349

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Db 1951 GGTGCTGCCGTGCCCCCAGGAGGAGATGACCAGTGCCTTGGCCACAATGCCGTTGACTA 2010

QY 363 xGluGlnIleLysIleLysIleGluAspAlaSerAsnProLeuLeuLeuLysArgAr 383

Db 2011 CGAGCAGATCAAGATAAAAAGATTGAAGATGCATCCAAACCCTCTGTCTGAAGAGCG 2070

QY 383 gLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396

Db 2071 GAAGAAAGCTCGGGCCCTGGAGGCTCGGGCTCTGGCCAC 2110

RESULT 6

AX335055

LOCUS AX335055 2258 bp DNA linear PAT 09-JAN-2002

DEFINITION Sequence 5564 from Patent WO0194629.

ACCESSION AX335055

VERSION AX335055.1 GI:18125774

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G., Horrigan,S., Soppet,D.R. and Weaver,Z.

TITLE Cancer gene determination and therapeutic screening using signature gene sets

JOURNAL Patent: WO 0194629-A 5564 13-DEC-2001; Avalon Pharmaceuticals (US)

FEATURES

source

1..2258

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

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Pred. No.: 3.31e-168 Length: 2258

Score: 1991.50 Matches: 396

Percent Similarity: 69.0% Conservative: 0

Best Local Similarity: 69.0% Mismatches: 0

Query Match: 94.6% Indels: 178

DB: 2 Gaps: 1

US-10-469-221-2 (1-396) x AX335055 (1-2258)

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Db 451 ACCCCTGCCCTGCCGACCCCCCGCGCAGCCGCGCCGCGCCCGCCGAGCAGTTCCCG 510

QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspAspTyrLys 60

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QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120

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QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140

Db 751 GAGAATCTGTACGCAGGGAGGAAGTGCCTGCTGATGTTCATGGAATGTTGGACGGTGA 810

QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160

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QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180

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Db 1291 CTGCTGAAAAACAGAGCCCAACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCCCTTGG 1350

QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340

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QY 341 AspLysGluArgTrpGluAspValLys----- 349

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QY 349 ----- 349

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Db	1411	GACAAGGAGCGGTGGGAGGATGTCAAGGGTGTCTTCATGACAAGAACAGCAGCAGGCC	1470
QY	349	-----	349
Db	1471	ACTTGGCTGACCAGGTTGTGAGCAGAGGATTCTGTGTTCTGTCTCCAAACTCAGTGTCTGTT	1530
QY	349	-----	349
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QY	349	-----	349
Db	1591	CTTCTCATTTTGCAGAAAGAAACTGAGGCCCGAGCGGAGGCAGTCTGTCTCAAGGTC	1650
QY	349	-----	349
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Db	1831	CCAGCCCGTCTTCTCTCTGTCTCCACCCCTGCGCGCTCACCTGCCCTTGTGTCTCTG	1890
QY	349	-----	349
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Db	1951	GGTGCTGCCGTGCCCCCAGGAGGAGATGACCAGTGCCCTTGGCCACAATGCGGTTGACTA	2010
QY	363	rGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLysArgAr	383
Db	2011	CGAGCAGATCAAGATAAAAGGATTGAAGATGCATCCAAACCCTCTGTCTGCTGAAGAGCG	2070
QY	383	gLysLysAlaArgAlaLeuGluAlaAlaAlaLeuAlaHis	396
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RESULT 8	
BC063064	
LOCUS	BC063064
DEFINITION	Mus musculus MAP kinase-activated protein kinase 2, mRNA (cDNA clone MGC:67217 IMAGE:5687007), complete cds.
ACCESSION	BC063064
VERSION	BC063064.1
KEYWORDS	MGC.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 2586) Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

TITLE	human and mouse cdna sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED	12477932
REFERENCE	2 (bases 1 to 2586)
AUTHORS	Strausberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (02-DEC-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library Preparation: M. Bento Soares, University of Iowa CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacques Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 124 Row: b Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

FEATURES
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gene

CDS

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ORIGIN

Alignment Scores:

Pred. No.: 1.02e-162 Length: 2586
Score: 1931.00 Matches: 368
Percent Similarity: 94.7% Conservative: 7
Best Local Similarity: 92.9% Mismatches: 7
Query Match: 91.7% Indels: 14
DB: 6 Gaps: 2

US-10-469-221-2 (1-396) x BC063064 (1-2586)

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QY	61	ValThrSerGlnValLeuGlyLysIleAsnGlyLysValLeuGlnIlePheAsnLys	80
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QY	381	LysArgArgLysLysAlaArgAlaLeuGluAlaAlaAlaLeuAlaHis	396
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RESULT 9

BC062048 2862 bp mRNA linear ROD 30-JUN-2004
LOCUS Rattus norvegicus MAP kinase-activated protein kinase 2, mRNA (cDNA
clone MGC:72264 IMAGE:5598069), complete cds.

ACCESSION

BC062048

VERSION

BC062048.1 GI:38303966

KEYWORDS

MGC.

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

REFERENCE

1 (bases 1 to 2862)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahey,J., Helton,E., Kettman,M., Madan,A., Young,A.C., Rodrigues,S.,

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,

Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

REFERENCE

2 (bases 1 to 2862)

Strausberg,R.

Direct Submission

Submitted (10-NOV-2003) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeff Green/Paturu Kondalah, NCI.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>

Contact: nisc_mgc@nhgri.nih.gov

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 137 Row: b Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 313424299.

FEATURES

source

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FEATURES
source
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ORIGIN

Alignment Scores:

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Score:	1930.00	Matches:	367
Percent Similarity:	94.7%	Conservative:	8
Best Local Similarity:	92.7%	Mismatches:	7
Query Match:	91.6%	Indels:	14
DB:	6	Gaps:	2

US-10-469-221-2 (1-396) x BC062048 (1-2862)

Qy	1	SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro	20
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Qy	21	ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro	40
Db	328	-----GCCCGCGCCAGCGCGCGCGCG-----TTCCCT	357

Qy 41 GlnPheHisValLysSerGlyLeuGlnIleLysAsnAlaIleAspTyrLys 60
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|||
Dd 358 CAGTTCCACGTCAAGTCGGGCCCTGCAGATCGAAAGAACGCCATCACCGACGACTACAAG 417
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QY	61	ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys	80
DB	418	GTCACCAAGTGGCTTGGCCCTAAGATGCTGCGGATCTTCGACAAG	477
QY	81	ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu	100
DB	478	AGAACCCAGCAAAATTCGCCCTAAAGATGCTGCAGGACTGTCCCAAGGCACGACAGAG	537
QY	101	ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr	120
DB	538	GTGGAGCTGCAGTGGAGGCCCTCCAGTGCCACACATCGTGACATCGTGGACGTCTAT	597
QY	121	GluAsnLeuTyrAlaGlyArgLysCysIleLeuValMetGluCysLeuAspGlyGly	140
DB	598	GAGAACCTGTATGCCGGGAGGAAGTGCTTCTGATGTTCATGGAGTGTCTCGATGGTGA	657
QY	141	GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer	160
DB	658	GAGCTCTTTAGTCGGATCCAGGACCGAGGAGCAGGCAATTCACAGAAAGAGAGGCATCA	717
QY	161	GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis	180
DB	718	GAGATCATGAAGAGCATCGGGAGGCCATCCAGTACCTGCACCTCTATCAACATCGCTCAC	777
QY	181	ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys	200
DB	778	CGGGACGTCGAAGCCCGAGAACCTCTTATACACTTCCAAAAGACCCCAATGCCATCCTGAAA	837
QY	201	LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys	220
DB	838	CTCACTGATTTGGCTTTGCCAAGGAACACCACGATCACAACTCTTTTGACCACTCCGTGT	897
QY	221	TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys	240
DB	898	TATACACGCTACTATGTGGCTCCGGAAGTACTGGGCCCCAGAGAAGTATGACAAGTCCTGT	957
QY	241	AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr	260
DB	958	GACATGTGGTCTTGGGTGTCATCATGTATATTTTGTGTGGGTATCCCCCTTCTAT	1017
QY	261	SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr	280
DB	1018	TCCAAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATTCGAATGGGCCAGTAT	1077
QY	281	GlupheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn	300
DB	1078	GAATTTCTTAACCCAGAAATGGTCAGAAGTATCAGAAGAAGTGAAGATGCTTATTCGGAAT	1137
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DB	1138	CTGCTGAAAACAGAGCCCAACCCAGAGAATGACCATCACAGAATTTCATGAACACCCCGTGG	1197
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QY	341	AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg	360
DB	1258	GACAAAGGAACGATGGGAGGATGTCAAGGAGGAGATGACCAAGTGCCCTTGGCCACGATGCGT	1317
QY	361	ValAspTyrGluGlnIleLysIleLysIleGluAspAlaSerAsnProLeuLeuLeu	380
DB	1318	GTCGACTATGAGCAGGTCAAGATAAAGATAGAGGACGCATCCCAACCCCTGTGCTTCTC	1377
QY	381	LysArgArgLysLysAlaArgAlaLeuGluAlaAlaAlaLeuAlaHis	396
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AY197741

LOCUS

DEFINITION

AY197741 2909 bp mRNA linear ROD 02-MAR-2003
Rattus norvegicus mitogen-activated protein kinase-activated
protein kinase-2 mRNA, complete cds.

ACCESSION AY197741
VERSION AY197741.1 GI:28629390
KEYWORDS .
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 2909)
AUTHORS Vician,L.J., Xu,G., Liu,W., Feldman,J.D., Machado,H.B. and Herschman,H.R.
TITLE MAPKAP Kinase-2 is a Primary Response Gene Induced by Depolarization in PC12 Cells and in Brain
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2909)
AUTHORS Vician,L.J., Xu,G. and Herschman,H.R.
TITLE Direct Submission
JOURNAL Submitted (16-DEC-2002) Biological Chemistry, UCLA, 611 Charles E. Young Dr. East, Los Angeles, CA 90095-1570, USA
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1463..2909
3'UTR
ORIGIN
Alignment Scores:
Pred. No.: 1.44e-162 Length: 2909
Score: 1930.00 Matches: 367
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Best Local Similarity: 92.7% Mismatches: 7
Query Match: 91.6% Indels: 14
DB: 6 Gaps: 2
US-10-469-221-2 (1-396) x AY197741 (1-2909)
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QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProProGlnGlnPhePro 40
DB 362 -----GCCCGCGCCAGCGCGCGCGCG-----TTCCCT 391
QY 41 GlnPheHisVallySerGlyLeuGlnIleLysLysAsnAlaIleIleAspAspTyrLys 60
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QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
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QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
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QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
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QY 361 ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeu 380
DB 1352 GTCGACTATGAGCAGGTCAAGATAAAGAAGATAGAGGACGCATCCAACCTCTGCTTCTC 1411
QY 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
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DEFINITION Mus musculus cDNA clone IMAGE:6432632.
ACCESSION BC052206
VERSION BC052206.1 GI:30354049
KEYWORDS .
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

CONSRM
TITLE

Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932

REFERENCE
AUTHORS

NIH MGC Project
Direct Submission
Submitted (01-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>

REMARK
COMMENT

Contact: cgabs-r@mail.nih.gov
Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)
cDNA Library Preparation: Catherine Lee, Endocrine Pancreas Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 111 Row: b Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 45544579.

FEATURES

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Best Local Similarity: 92.7% Mismatches: 8

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RESULT 14

DD182194

LOCUS DD182194 1305 bp DNA linear PAT 19-DEC-2005

DEFINITION Methods and Compositions for Protein Expression and Purification.

ACCESSION DD182194

VERSION DD182194.1 GI:83957055

KEYWORDS JP 2005514025-A/15.

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 1305)

AUTHORS Malakhova,O.A., Butt,T.R., Tran,H.T., Malakhov,M.P. and Weeks,S.D.

TITLE Methods and Compositions for Protein Expression and Purification

JOURNAL Patent: JP 2005514025-A 15 19-MAY-2005;

Tauseef Butt,Stephen Weeks,Hiep Tran,Oxana Malakhova, Micheal Malakhov

COMMENT OS Artificial Sequence

PN JP 2005514025-A/15

PD 19-MAY-2005

PF 07-JAN-2003 JP 2003557532

PR 07-JAN-2002 US 60/346449

PI oxana a malakhova,tauseef r butt,hiep t tran,micheal p pi malakhov,

PI stephen d weeks

CC Synthetic Sequence

FH Key Location/Qualifiers.

source 1. .1305

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ORIGIN

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Score: 1729.00 Matches: 327

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Best Local Similarity: 100.0% Mismatches: 0

Query Match: 82.1% Indels: 0

DB: 2 Gaps: 0

US-10-469-221-2 (1-396) x DD182194 (1-1305)

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Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160

Db 622 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTCACAGAAAGAGAAGCATCC 681

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Db 1282 GTTGACTACGAGCAGATCAAG 1302

RESULT 15

CS214061 1168 bp DNA linear PAT 15-DEC-2005

LOCUS CS214061

DEFINITION Sequence 3380 from Patent WO2005111246.

ACCESSION CS214061

VERSION CS214061.1 GI:83681911

KEYWORDS Cricetulus longicaudatus (long-tailed hamster)

SOURCE Cricetulus longicaudatus

ORGANISM Cricetulus longicaudatus

REFERENCE 1

AUTHORS Melville,M.W.

TITLE Oligonucleotide arrays to monitor gene expression and methods for making and using same

JOURNAL Patent: WO 2005111246-A 3380 24-NOV-2005;

Wyeth (US)

FEATURES Location/Qualifiers

source 1. .1168

/organism="Cricetulus longicaudatus"

ORIGIN

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DB: 2

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Matches: 324
Conservative: 4
Mismatch: 1
Indels: 0
Gaps: 0

US-10-469-221-2 (1-396) x CS214061 (1-1168)

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Db 1 CTGGGCATCAATGGGAAGGTGCTGCGGATCTTCGACAAGAGAACCCAGCAAAAATTGCCC 60

QY 88 LeuLysMetLeuGlnAspCysProLysAlaArgGluValGluLeuHisTrpArgAla 107
Db 61 CTGAAGATGCTCCAGGACTGTCCGAAGGCCACGACAGAGGTGGAGCTGCACTGGAGGGCC 120

QY 108 SerGlnCysProHisIleValArgIleValAspValTyrGluAsnLeuTyrAlaGlyArg 127
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QY 128 LysCysLeuLeuIleValMetGluCysLeuAspGlyGlyGluLeuPheSerArgIleGln 147
Db 181 AAGTGCCTGCTGATTGTCATGGAGTGTCTCGATGTGGAGAGCTCTTTAGTCGAATCCAG 240

QY 148 AspArgGlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMetLysSerIleGly 167
Db 241 GACCGAGGAGACCAGGCATTACAGAAAGAGAGCGGTCAGAAATCATGAAGAGCATTGGT 300

QY 168 GluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHisArgAspValLysProGluAsn 187
Db 301 GAGGCCATCCAGTATTGCACTCAATCAACATTGCTCATCGGGATGTCAAAGCCTGAGAAC 360

QY 188 LeuLeuTyrThrSerLysArgProAsnAlaIleLeuLysLeuThrAspPheAla 207
Db 361 CTCTTATATACTTCCAAAAGGCCCAATGCCATTCTGAAACTCACTGATTTTGGCTTTGCC 420

QY 208 LysGluThrThrSerHisAsnSerLeuThrProCysTyrThrProTyrTyrValAla 227
Db 421 AAGGAAACCACCACTGTCACAACTCTCTGACCACTCCGTGTTATACACCATACTACGTAGCT 480

QY 228 ProGluValLeuGlyProGluLysTyrAspLysSerCysAspMetTrpSerLeuGlyVal 247
Db 481 CCGGAAGTGTGGTCCAGAGAAGTATGACAAATCCTGTGACATGTGGTCCTTGGGTGTC 540

QY 248 IleMetTyrIleLeuLeuCysGlyTyrProPheTyrSerAsnHisGlyLeuAlaIle 267
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QY 288 SerGluValSerGluGluValLysMetLeuIleArgAsnLeuLeuLysThrGluProThr 307
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QY 328 ProGlnThrProLeuHisThrSerArgValLeuLysGluAspLysGluArgTrpGluAsp 347
Db 781 CCTCAGACTCCACTGCACACCAGCCGTGTCTGAAAGGAGGACAAGGAACGGTGGGAGGAT 840

QY 348 ValLysGluGluMetThrSerAlaLeuAlaThrMetArgValAspTyrGluGlnIleLys 367
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QY 368 IleLysLysIleGluAspAlaSerAsnProLeuLeuLysArgArgLysLysAlaArg 387
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QY 388 AlaLeuGluAlaAlaAlaLeuAlaHis 396
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Search completed: June 19, 2006, 16:48:42
Job time : 7503 secs

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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 19, 2006, 15:07:48 ; Search time 6132 Seconds
(without alignments)
5416.843 Million cell updates/sec

Title: US-10-469-221-2
Perfect score: 2106
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1931	91.7	2674	6 AK155171	AK155171 Mus muscu
2	1577	74.9	901	8 CR980921	CR980921 CR980921
3	1550	73.6	941	3 BQ884713	BQ884713 AGENCOURT
4	1500	71.2	850	9 DN107605	DN107605 1105067 M

5	1398	66.4	780	14	AY410229	AY410229 Homo sapi
6	1396	66.3	1182	9	DN666480	DN666480 CFW32-D05
7	1393	66.1	780	14	AY410231	AY410231 Mus muscu
8	1393	66.1	920	10	DT404291	DT404291 JGI_CABI6
9	1391	66.0	1149	14	AY403347	AY403347 Homo sapi
10	1391	66.0	1799	6	CR606251	CR606251 full-leng
11	1384	65.7	3003	6	BC068497	BC068497 Homo sapi
12	1361	64.6	1155	14	AY403349	AY403349 Mus muscu
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16	1359	64.5	842	5	CF617043	CF617043 AGENCOURT
17	1347	64.0	2747	6	AK144637	AK144637 Mus muscu
18	1344	63.8	902	10	DV928789	DV928789 LB03014.C
19	1338	63.5	776	3	BU609266	BU609266 UI-M-FR0-
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22	1328	63.1	883	8	CR440918	CR440918 CR440918
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26	1287	61.1	728	5	CF725542	CF725542 UI-M-GZ0-
27	1286	61.1	751	4	CB169658	CB169658 RUC603000
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ALIGNMENTS

RESULT 1	AK155171	2674 bp	mRNA	linear	HTC 21-SEP-2005
LOCUS	Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630205L24 product:MAP kinase-activated protein kinase 2, full insert sequence.				
DEFINITION					
ACCESSION	AK155171				
VERSION	AK155171.1 GI:74199084				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchoptoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.				
	1				
	Carninci, P. and Hayashizaki, Y.				
	High-efficiency full-length cDNA cloning				
AUTHORS	Meth. Enzymol. 303, 19-44 (1999)				
	10349636				
TITLE	2				
	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
	Genome Res. 10 (10), 1617-1630 (2000)				
PUBMED	11042159				
	3				
REFERENCE	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,				
	1				

Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861

TITLE

JOURNAL

PUBMED

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4 Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

11217851

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5 Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

FANTOM Consortium

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420 (6915), 563-573 (2002)

12466851

REFERENCE

AUTHORS

6 Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E.,

Ambesi-Impimbato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminiecchi,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S., Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavese,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiyura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

CONSRTM

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

RIKEN Genome Exploration Research Group

Antisense transcription in the mammalian transcriptome

Science 309 (5740), 1564-1566 (2005)

16141073

REFERENCE

AUTHORS

8 (bases 1 to 2674)
Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submision

Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa, 230-0045, Japan (E-mail:genome-res@gs.riken.jp,

URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,

Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics

Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome

Trust/MRC building Addenbrookes Hospital Cambridge) whose

assistance we gratefully acknowledge.

COMMENT

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES

source
Location/Qualifiers
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EVLGPEKYDKSCDMWSLGVIMYILLCGYPFFYSNHNGLAISPGMKTRIRMQYEFNP
E
WSEVSEEVKMLIRNLLKTEPTQRTITEFMNHPWIMQSTKVPOTPLHTSRVLKEDKER
WEDVKEMTSALATMRVDYEQIKIKKIEDASNPLLLKRRKKARAVEDAALAH"

CDS

Alignment Scores:

Pred. No.: 2,56e-155 Length: 2674
Score: 1931.00 Matches: 368
Percent Similarity: 94.7% Conservative: 7
Best Local Similarity: 92.9% Mismatches: 7
Query Match: 91.7% Indels: 14
DB: 6 Gaps: 2

US-10-469-221-2 (1-396) x AK155171 (1-2674)

QY 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20
||| |||||:::||||| |||||:::||||| |||||
DB 298 TCTCCGGGCCAGACTCCGGCGCCTTTCCCGAGCCCTCCACCGCCA----- 345
QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProProGlnGlnPhePro 40
||| |||||:::||||| |||||:::||||| |||||
DB 346 -----GCCCGGGCCAGCGCGCGCGCG-----TTCCCC 375
QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspTyrLys 60
||| |||||:::||||| |||||:::||||| |||||
DB 376 CAGTTCCACGTCAGTCGGGCCTGCAGATCCGAAAGAACGCCATCACCGAGCTACAAG 435
QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
||| |||||:::||||| |||||:::||||| |||||
DB 436 GTCACCAAGCCAGTGTGGCCTGGGCATCAACGGGAAGGTGCTGCGGATCTTCGACAAG 495
QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
||| |||||:::||||| |||||:::||||| |||||
DB 496 AGAACCCAGCAAAAATTCCCCCTAAAGATGCTCCAGGACTGTCCGAAGCGCGCAGAGAG 555
QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
||| |||||:::||||| |||||:::||||| |||||
DB 556 GTGGAGCTGCACCTGGAGGGCCTCCCGAGTGCACACACATTGTGCACATCGTGGATGTCTAT 615
QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
||| |||||:::||||| |||||:::||||| |||||
DB 616 GAGAACCTGTATGCCGGGAGGAAGTGCCTGTGATTGTCTATGGAGTGTCTCGATGGTGA 675
QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
||| |||||:::||||| |||||:::||||| |||||
DB 676 GAGCTCTTTAGTCGAATCCAGGACCGAGGACCAAGGCATTTCACAGAAAGAGAGGCGTCA 735
QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
||| |||||:::||||| |||||:::||||| |||||

Best Local Similarity: 96.2%				Mismatches:	4
Query Match: 73.6%				Indels:	4
DB:				Gaps:	0
US-10-469-221-2 (1-396) x BQ884713 (1-941)					
QY	76	GlnIlePheAsnLysArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysPro	95		
Db	2	CGGATCTTCGACAAGAGAACCCAGCAAAATTCGCCCTAAAGATGCTCCAGGACTGTCCG	61		
QY	96	LysAlaArgArgGluValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArg	115		
Db	62	AAGGCGCGCAGAGAGGTGGAGCTGCACTGGAGGCCTCCAGTGCCTCCACACATTGTGCAC	121		
QY	116	IleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGlu	135		
Db	122	ATCGTGGATGTCTATGAGAACCTGTATGCCGGGAGGAAGTGCCTGCTGATTGTCATGGAG	181		
QY	136	CysLeuAspGlyGlyGluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThr	155		
Db	182	TGTCTCGATGGTGGAGAGCTCTTTTAGTCGAATCCAGGACCGAGGAGACCGCATTCACA	241		
QY	156	GluArgGluAlaSerGluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSer	175		
Db	242	GAAGAGAGGCGTCAGAGATCATGAAGAGCATCGCGGAGGCCATCCAGTACCTGCACTCG	301		
QY	176	IleAsnIleAlaHisArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgPro	195		
Db	302	ATCAACATTGCTCACCGGATGTCAAGCCTGAGAACCTCTTATATACTTCCAAAAGGCC	361		
QY	196	AsnAlaIleLeuLysLeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSer	215		
Db	362	AATGCCATTTGAAACTCACTGATTTTGGCTTTGCCAAGGAAACCCAGTCACAACTCT	421		
QY	216	LeuThrThrProCysTyrThrProTyrTyrValAlaProGluValLeuGlyProGluLys	235		
Db	422	TTGACCACTCCGTGTTATACACCATACTATGTGGTCCGGAAGTCTCGGCCCGGAGAAG	481		
QY	236	TyrAspLysSerCysAspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGly	255		
Db	482	TATGACAAGTCTGTGACATGTGTCTTGGTGTTCATCATGTATATTTGTGTGGG	541		
QY	256	TyrProProPheTyrSerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgile	275		
Db	542	TATCCCCCTTCTATTCCAATCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGTATT	601		
QY	276	ArgMetGlyGlnTyrGluPheProAsnProGluTrpSerGluValSerGluValLys	295		
Db	602	CGAATGGGCCAGTATGAATTTCTTAACCGGAGTGGTCAGAAGTATCAGAAGAAGTGAAG	661		
QY	296	MetLeuIleArgAsnLeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPhe	315		
Db	662	ATGCTTATCCGGAATCTGCTAAAAACAGAGCCCCACCCAGAGAAATGACCATCACAGAATTC	721		
QY	316	MetAsnHisProTrpIleMetGlnSerThrLysValProGlnThrProLeuHisThrSer	335		
Db	722	ATGAACCAACCCTGGATCATGCAATCTACGAAGGTCCCTCAGACTCCACTGCACACCAGC	781		
QY	336	-ArgValLeuLysGluAspLysGluArg-TrpGluAspValLysGlu-GluMetThrSer	354		
Db	782	CNGTGTCTCGAAGGAGGACAAAGGAACGGATGGGAGGATGTCAAGGAGGGAGATGACCAGT	841		
QY	355	AlaLeu-AlaThrMetArgValAspTyrGluGlnIleLysIleLysIleGluAspAl	374		
Db	842	GCCTTGGGCCACGATCGTGTGACTATGAGCAGATCCAGATAAAGAAGATAGAAGACGC	901		
QY	374	aSerAsnProLeuLeuLysArgArgLysLys	385		
Db	902	ATCCAACCCCTCTGCTTCTCAAGAGCGGGGAAGAAG	935		
RESULT 4					
DN107605					
LOCUS					
DN107605 850 bp mRNA linear EST 14-FEB-2005					

DEFINITION		1105067 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.	
ACCESSION		DN107605	
VERSION		DN107605.1 GI:59782868	
KEYWORDS		EST.	
SOURCE		Sus scrofa (pig)	
ORGANISM		Sus scrofa	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.	
REFERENCE		1 (bases 1 to 850)	
AUTHORS		Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A., Nonneman,D.J., Wray,J.E. and Keele,J.W.	
TITLE		Porcine EST collection using a normalized library constructed from embryos representing early developmental stages	
JOURNAL		Unpublished (2003)	
COMMENT		Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329. Plate: HHY8003 row: B column: 15 Seq primer: GTAATACGACTCACTATAGGG.	
FEATURES		Location/Qualifiers	
		1..850	
		/organism="Sus scrofa"	
		/mol_type="mRNA"	
		/db_xref="taxon:9823"	
		/tissue_type="pooled"	
		/lab_host="DH10B"	
		/clone_lib="MARC 4PIG"	
		/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."	
ORIGIN			
Alignment Scores:			
Pred. No.:		7.9e-119	Length: 850
Score:		1500.00	Matches: 281
Percent Similarity:		100.0%	Conservative: 2
Best Local Similarity:		99.3%	Mismatches: 0
Query Match:		71.2%	Indels: 0
DB:		9	Gaps: 0
US-10-469-221-2 (1-396) x DN107605 (1-850)			
QY	52	LysAsnAlaIleIleAspAspTyrLysValThrSerGlnValLeuGlyLeuGlyIleAsn	71
Db	2	AAGAAAGCCATCATCGACGACTACAAGGTCAACCCAGGTCAACCCAGGTCTGGGACTGGGCATCAAC	61
QY	72	GlyLysValLeuGlnIlePheAsnLysArgThrGlnGluLysPheAlaLeuLysMetLeu	91
Db	62	GGGAAAGTTTTCAGATCTTCAACAAGAGGACCCAGGAGAAATTCGCCCTAAAAATGCTT	121
QY	92	GlnAspCysProLysAlaArgArgGluValGluLeuHisTrpArgAlaSerGlnCysPro	111
Db	122	CAGACTGTCCCAAGGCCCGCGAGGTGGAGTGCATCTGGCGGGCTCCAGTGCCCCA	181
QY	112	HisIleValArgIleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCysLeuLeu	131
Db	182	CACATCGTCGGATCGTGGACGCTCTATGAGAACCTGTACGCGGGAGGAAGTGCCTACTG	241
QY	132	IleValMetGluCysLeuAspGlyGlyGluLeuPheSerArgIleGlnAspArgGlyAsp	151
Db	242	ATCGTCATGGAGTGTGATGGTGGAGAACTCTTTAGCCGAATCCAGGACCGAGGAGAC	301
QY	152	GlnAlaPheThrGluArgGluAlaSerGluIleMetLysSerIleGlyGluAlaIleGln	171
Db	302	CAAGCGTTCACAGAAAGAGAGGCATCAGAAATCATGAAGAGCATTTGGTGAGCCATCCAG	361

QY	172	TyrLeuHisSerIleAsnIleAlaHisArgAspValLysProGluAsnLeuTyrThr	191
Db	362	TATTTGCACTCAATCAACATTGCTCATCGAGACGTCGAAGCCTGAGAAATCTCTTGTACACC	421
QY	192	SerLysArgProAsnAlaIleLeuLysLeuThrAspPheGlyPheAlaLysGluThrThr	211
Db	422	TCCAAAGGCCCAACGCCATTCTCAAACTCACCGATTTTGGCTTTGCCAAGGAACCAACC	481
QY	212	SerHisAsnSerLeuThrThrProCysTyrThrProTyrTyrValAlaProGluValLeu	231
Db	482	AGCCACAACACTGACCACTCCCTGTTACACGCCGTACTATGTGGCTCCAGAAGTGCTG	541
QY	232	GlyProGluLysTyrAspLysSerCysAspMetTipSerLeuGlyValIleMetTyrIle	251
Db	542	GGCCCCGAGAAGTATGACAAAGTCCTGTGACATGTGTCCTTGGGTGCATCATGTACATC	601
QY	252	LeuLeuCysGlyTyrProProPheTyrSerAsnHisGlyLeuAlaIleSerProGlyMet	271
Db	602	CTGCTGTGTGGGTACCCCCCTTCTATTCCAACCATGGCCTCGCCATCTCTCCCGGCATG	661
QY	272	LysThrArgIleArgMetGlyGlnTyrGluPheProAsnProGluTyrPheSerGluValSer	291
Db	662	AAGAGTCGCATCCGAATGGCCAGTATGAATTTCCCAACCCGGAAATGGTCAGAAATATCA	721
QY	292	GluGluValLysMetLeuIleArgAsnLeuLysThrGluProThrGlnArgMetThr	311
Db	722	GAAGAAGTGAAGATGCTCATCCGGAACCTGCTGAAGACAGAGCCACCCAGAGGATGACC	781
QY	312	IleThrGluPheMetAsnHisProTyrIleMetGlnSerThrLysValProGlnThrPro	331
Db	782	ATCACCGAGTTTCATGAACCAACCCCTGGATCATGCAATCTACGAAGGTCCCTCAAACCCCA	841
QY	332	LeuHisThr	334
Db	842	CTGCACACC	850
RESULT 5	AY410229		
LOCUS	AY410229 Homo sapiens MAPKAPK2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.		
DEFINITION	AY410229 Homo sapiens (human)		
ACCESSION	AY410229.1 GI:39766197		
VERSION	GSS.		
KEYWORDS	Homo sapiens		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 780)		
AUTHORS	Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCE	2 (bases 1 to 780)		
AUTHORS	Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
FEATURES	Location/Qualifiers		
source	1..780		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
gene	<1..>780		
	/gene="MAPKAPK2"		
	/locus_tag="HCM3821"		
ORIGIN			
Alignment Scores:			
Pred. No.:	4.36e-110	Length:	780
Score:	1398.00	Matches:	260
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	66.4%	Indels:	0
DB:	14	Gaps:	0
US-10-469-221-2 (1-396) x AY410229 (1-780)			
QY	90	MetLeuGlnAspCysProLysAlaArgArgGluValGluLeuHisTrpArgAlaSerGln	109
Db	1	ATGCTTCAGGACTGCCCAAGGCCCGCAGGAGGTGGAGTGCACCTGGCGGCCTCCCCAG	60
QY	110	CysProHisIleValArgIleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCys	129
Db	61	TGCCGCGACATCGTACGGATCGTGGATGTGTACGAGAACTCTTAGCCGAATCCAGGATCGA	120
QY	130	LeuLeuIleValMetGluCysLeuAspGlyGlyGluLeuPheSerArgIleGlnAspArg	149
Db	121	CTGCTGATTGTCAATGGAATGTTGGACGGTGGAGAACTCTTAGCCGAATCCAGGATCGA	180
QY	150	GlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMetLysSerIleGlyGluAla	169
Db	181	GGAGACCAGGCATTTCACAGAAAGAGAGCATCCGAAATCATGAAGAGCATCGGTGAGGCC	240
QY	170	IleGlnTyrLeuHisSerIleAsnIleAlaHisArgAspValLysProGluAsnLeuLeu	189
Db	241	ATCCAGTATCTGCATTCAATCAATCAATGCCCATCGGGATGTCAGGCCTGAGAAATCTCTTA	300
QY	190	TyrThrSerLysArgProAsnAlaIleLeuLysLeuThrAspPheGlyPheAlaLysGlu	209
Db	301	TACACTCCAAAGGCCCAACGCCATCCTGAAACTCCTGAAACTCCTGACTTTGGCTTTGCCAAGGAA	360
QY	210	ThrThrSerHisAsnSerLeuThrThrProCysTyrThrProTyrTyrValAlaProGlu	229
Db	361	ACCACGAGCCACAACCTCTTTGACCACCTCCTTGTATTATACCCGTACTATGTGGTCTCCAGAA	420
QY	230	ValLeuGlyProGluLysTyrAspLysSerCysAspMetTrpSerLeuGlyValIleMet	249
Db	421	GTGCTGGGTCCAGAGAAGTATGACAAAGTCCTGTGACATGTGGTCCCTGGGTGTTCATCATG	480
QY	250	TyrIleLeuLeuCysGlyTyrProProPheTyrSerAsnHisGlyLeuAlaIleSerPro	269
Db	481	TACATCCTGCTGTGTGGGTATCCCCCTTCTACTCCAACCCACGCGCTTGCCATCTCTCCG	540
QY	270	GlyMetLysThrArgIleArgMetGlyGlnTyrGluPheProAsnProGluTyrSerGlu	289
Db	541	GGCATGAAGACTCGCATCCGAATGGGCCAGTATGAATTTCCCAACCCAGAATGGTCAGAA	600
QY	290	ValSerGluGluValLysMetLeuIleArgAsnLeuLeuLysThrGluProThrGlnArg	309
Db	601	GTATCAGAGGAAGTGAAGATGCTCATTCGGAATCTGCTGAAAAACAGAGCCCCCAGAGA	660
QY	310	MetThrIleThrGluPheMetAsnHisProTyrIleMetGlnSerThrLysValProGln	329
Db	661	ATGACCATCACCGAGTTTATGAACCAACCCTTGGATCATGCAATCAACAAAGGTCCCTCAA	720
QY	330	ThrProLeuHisThrSerArgValLeuLysGluAspLysGluArgTrpGluAspValLys	349
Db	721	ACCCCACTGCACACCAGCCGGTCTCTGAAGGAGGACAAGGAGCGGTGGAGGATGTCAAG	780
RESULT 6	DN666480		
LOCUS	DN666480 1182 bp mRNA linear EST 29-MAR-2005		
DEFINITION	CFW32-D05.y1d-s SHGC-CFW Gasterosteus aculeatus cDNA clone		
ACCESSION	CFW32-D05 5', mRNA sequence.		
	DN666480		

VERSION	DN666480.1	GI:61986536	
KEYWORDS	EST.		
SOURCE	Gasterosteus aculeatus (three spined stickleback)		
ORGANISM	Gasterosteus aculeatus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.		
REFERENCE	1 (bases 1 to 1182)		
AUTHORS	Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.		
TITLE	Expressed sequence tags from Gasterosteus aculeatus		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Grimwood, Jane Stanford Human Genome Center Stanford University School of Medicine 975 S California Ave, Palo Alto, CA 94304, USA Tel: 650 320 5917 Fax: 650 320 5801 Email: jane@shgc.stanford.edu Plate: 32		
FEATURES	High quality sequence stop: 831.		
source	Location/Qualifiers		
	1..1182		
	/organism="Gasterosteus aculeatus"		
	/mol_type="mRNA"		
	/strain="Conner Creek sticklebacks, WA USA"		
	/db_xref="taxon:69293"		
	/clone="CPW32-D05"		
	/sex="mixed male and female"		
	/tissue_type="gills"		
	/dev_stage="adult"		
	/lab_host="DH10B (T1 phage resistant)"		
	/clone_lib="SHGC-CFW"		
	/note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTCTAGATCGGAGCGCGCCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC'(where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: http://www.openbiosystems.com/cdna_library_construction_fa_q.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems: http://www.openbiosystems.com/stickleback "		
ORIGIN			
Alignment Scores:			
Pred. No.:	1.12e-109	Length:	1182
Score:	1396.00	Matches:	262
Percent Similarity:	93.6%	Conservative:	18
Best Local Similarity:	87.6%	Mismatches:	18
Query Match:	66.3%	Indels:	1
DB:	9	Gaps:	0
US-10-469-221-2 (1-396) x DN666480 (1-1182)			
Qy	90	MetLeuGlnAspCysProLysAlaArgGluValGluLeuHisTrpArgAlaSerGln	109
Db	2	ATGCTGCAGGATTGTGCCAAGGCCCGTAGGAACTGGAGCTGCACCTGGAGGCTTCTCCC	61
Qy	110	CysProHisIleValArgIleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCys	129
Db	62	TGTGCCAACATTGTGGCATCATTGATGTCTATGAGAACCTCTATCAGACGAGGAAGTGT	121
Qy	130	LeuLeuIleValMetGluCysLeuAspGlyGlyGluLeuPheSerArgIleGlnAspArg	149
Db	122	CTGCTTATTGTTCATGGAGTGCATGGATGGTGGTGAGCTTTTAGTCGAATCCAGGACAGA	181
Qy	150	GlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMetLysSerIleGlyGluAla	169
Db	182	GGAGATCAGGCTTTCACAGAGCGAGAGGCGTCTGACATCATGAAAAACATCGGAGGCC	241
Qy	170	IleGlnTyrLeuHisSerIleAsnIleAlaHisArgAspValLysProGluAsnLeuLeu	189
Db	242	ATTCTAGTTCTTCATGCCGTCAACATTGCTCACAGAGACGTCAAGCCACAGAACTTACTG	301
Qy	190	TyrThrSerLysArgProAsnAlaIleLeuLysLeuThrAspPheGlyPheAlaLysGlu	209
Db	302	TATTCCTCAAAGAGGCCCAACGCCCTGCTCAAACTCACAGATTTTGGCTTTGCCAAGGAA	361
Qy	210	ThrThrSerHisAsnSerLeuThrThrProCysTyrThrProTyrTyrValAlaProGlu	229
Db	362	ACCACCTCCACAACACTCTTTAGCTACTCCGTGTACACCCCTACTATGTGTGCTCCAGAA	421
Qy	230	ValLeuGlyProGluLysTyrAspLysSerCysAspMetTrpSerLeuGlyValIleMet	249
Db	422	GTTCCTGGCCACAGAGAAATATGACAAGTCATGTGATGTGGTCACTGGTGTCTATTATG	481
Qy	250	TyrIleLeuLeuCysGlyTyrProProPheTyrSerAsnHisGlyLeuAlaIleSerPro	269
Db	482	TATATCCTGTGTGTGGATACCCCTCCTTTTATTCAAAACCACGGTTTAGCCATCTCTCCT	541
Qy	270	GlyMetLysThrArgIleArgMetGlyGlnTyrGluPheProAsnProGluTrpSerGlu	289
Db	542	GGGATGAAGAGAGGATCAGGATGGGCCAATATGAGTTTCCAAACCCCTGAGTGGTCTGAC	601
Qy	290	ValSerGluGluValLysMetLeuIleArgAsnLeuLeuLysThrGluProThrGlnArg	309
Db	602	GTATCAGAGGAAGCAAAACAACACTGATTAGGACTCTCTTAAGACTGAGCCAACGCAGAGG	661
Qy	310	MetThrIleThrGluPheMetAsnHisProTrpIleMetGlnSerThrLysValProGln	329
Db	662	ATGACCATCACCGAATTTCATGAATAATCCCTGGATCAATCAATCGATGGAGGTCCCCAG	721
Qy	330	ThrProLeuHisThrSerArgValLeuLysGluAspLysGluArgTrpGluAspValLys	349
Db	722	ACCCCACTTCACACCAGCCGGGTGCTAAAGGAGGAGGACCGCTGNGAGGATGTCAAG	781
Qy	350	GluGluMetThrSerAlaLeuAlaThrMetArgValAspTyrGluGlnIleLysIleLys	369
Db	782	GAGGAATGACCACTGCCTTGGNCACAATGAGAGTCGACTACGAGCAAAATNCAGATCAAG	841
Qy	370	LysIleGluAspAlaSer-AsnProLeuLeuLeuLysArgArgLysLysAlaArg	387
Db	842	ACCATTGAGGACTCGACCCCAATCCCTGCTAAACAAAAAGAGAAAGAAAGCCCCGT	896
RESULT 7			
AY410231			
LOCUS	AY410231	780 bp	DNA linear GSS 16-DEC-2003
DEFINITION	Mus musculus MAPKAPK2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.		
ACCESSION	AY410231		
VERSION	AY410231.1	GI:39766199	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 780)		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		

JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 780)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1..780
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
gene <1..>780
/gene="MAPKAPK2"
/locus_tag="HCM3821"
ORIGIN
Alignment Scores:
Pred. No.: 1.18e-109 Length: 780
Score: 1393.00 Matches: 259
Percent Similarity: 99.6% Conservative: 0
Best Local Similarity: 99.6% Mismatches: 1
Query Match: 66.1% Indels: 0
DB: 14 Gaps: 0
US-10-469-221-2 (1-396) x AY410231 (1-780)
Qy 90 MetLeuGlnAspCysProLysAlaArgGluValGluLeuHisTrpArgAlaSerGln 109
Db 1 ATGCTCCAGGACTGCCGAAGGCGCGAGAGGTGGAGCTGCACCTGGAGGGCCTCCAG 60
Qy 110 CysProHisIleValArgIleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCys 129
Db 61 TGCCACACATTGTGCACATCGTGGATGCTATGAGAACCTGTATGCCGGAGGAAGTGC 120
Qy 130 LeuLeuIleValMetGluCysLeuAspGlyGlyGluLeuPheSerArgIleGlnAspArg 149
Db 121 CTGCTGATTGTCATGGAGTGCTCGATGGTGGAGAGCTCTTTAGTCGAATCCAGGACCGA 180
Qy 150 GlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMetLysSerIleGlyGluAla 169
Db 181 GGAGACCAGGCATTACAGAAAGAGAGGCGTCAGAGATCATGAAGAGCATCGCGGAGGCC 240
Qy 170 IleGlnTyrLeuHisSerIleAsnIleAlaHisArgAspValLysProGluAsnLeuLeu 189
Db 241 ATCCAGTACCTGCACTCGATCGATCAACATTGCTCACCGGGATGTCAAGCCTGAGAACCTCTTA 300
Qy 190 TyrThrSerLysArgProAsnAlaIleLeuLysLeuThrAspPheGlyPheAlaLysGlu 209
Db 301 TATACTTCCAAAAGGCCCAATGCCATTTTGAAACTCACTGATTTTGGCTTTGCCAAGGAA 360
Qy 210 ThrThrSerHisAsnSerLeuThrThrProCysTyrThrProTyrTyrValAlaProGlu 229
Db 361 ACCACCAGTCACAACTCTTTTGACCACCTCCGCTTATACACCATACTATGTGGCTCCGAA 420
Qy 230 ValLeuGlyProGluLysTyrAspLysSerCysAspMetTrpSerLeuGlyValIleMet 249
Db 421 GTCCTGGGCCCCGAGAAGATATGACAACTCCTGTGACATGTGGTCCTTGGGTGCATCATG 480
Qy 250 TyrIleLeuLeuCysGlyTyrProProPheTyrSerAsnHisGlyLeuAlaIleSerPro 269
Db 481 TATATTTTGTGTGGGTATCCCCCCTTCTATTCCAATCACGGCCTTGCCATCTCTCCG 540
Qy 270 GlyMetLysThrArgIleArgMetGlyGlnTyrGluPheProAsnProGluTrpSerGlu 289
Db 541 GGCATGAAGACTCGTATTTCGAATGGGCCAGTATGAATTTTCCTAACCCGAGTGGTCAGAA 600
Qy 290 ValSerGluGluValLysMetLeuIleArgAsnLeuLeuLysThrGluProThrGlnArg 309

Db 601 GTATCAGAAAGAGTGAAGATGCTTATCCGGAATCTGCTAAAAACAGAGCCACCCAGAGA 660
Qy 310 MetThrIleThrGluPheMetAsnHisProTrpIleMetGlnSerThrLysValProGln 329
Db 661 ATGACCATCACAGAATTTCATGAACCAACCCCTGGATCATGCAATCTACGAAGGTCCCTCAG 720
Qy 330 ThrProLeuHisThrSerArgValLeuLysGluAspLysGluArgTrpGluAspValLys 349
Db 721 ACTCCACTGCACACCAGCCGTGTCTGAAGGAGGACAAGGAACGATGGGAGGATGTCAAG 780
RESULT 8
LOCUS DT404291 920 bp mRNA linear EST 25-AUG-2005
DEFINITION JGI CABI6679.fwd NIH XGC tropOv11 Xenopus tropicalis cDNA clone IMAGE:7859151 5', mRNA sequence.
ACCESSION DT404291
VERSION DT404291.1 GI:73790488
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae; Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 920)
AUTHORS Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.
TITLE DOE Joint Genome Institute Xenopus tropicalis EST project
JOURNAL Unpublished (2004)
COMMENT Other_ESTs: JGI CABI6679.rev
Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Robert M. Grainger
CDNA Library Preparation: Bruce Blumberg Laboratory, University of California, Irvine
CDNA Library Arrayed by: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LNL:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
Plate: CABI 0069 row: n column: 13
High quality sequence stop: 783.
FEATURES Location/Qualifiers
source 1..920
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/strain="N6 (Nigerian 6th generation inbred)"
/db_xref="taxon:8364"
/clone="IMAGE:7859151"
/sex="female"
/tissue_type="Oviduct"
/dev_stage="Adult"
/lab_host="ElectroMAX DH10B T1 Phage Resistant cells"
/clone_lib="NIH XGC tropOv11"
/note="Vector: pCS107; Site_1: EcoRI; Site 2: XhoI; The library was prepared from 5 ug of poly A+ RNA by oligo-dT priming (5'-ACTAGTGGCGCGCTAGCCCTCGAGTTTTTTTTTTTTTTT-3') and Stratascript reverse transcriptase. After ligation of EcoRI adapters (5'-AATTCGGCAGGAG-3') followed by kinasing adapters and by XhoI digestion, the cDNA was size selected by chromatography on Sepharose CL-2B columns and fractions containing cDNAs larger than 1000 bp were ligated into EcoRI/XhoI-digested pCS107. Reference for library construction: Current Genomics 4, 635-644. Library

constructed by Michelle Tabb and Bruce Blumberg (Dept of Developmental and Cell Biology, University of California, Irvine)."

ORIGIN

Alignment Scores:
Pred. No.: 1.46e-109 Length: 920
Score: 1393.00 Matches: 265
Percent Similarity: 93.0% Conservative: 16
Best Local Similarity: 87.7% Mismatches: 21
Query Match: 66.1% Indels: 1
DB: 10 Gaps: 0

US-10-469-221-2 (1-396) x DT404291 (1-920)

QY 37 GlnGlnPheProGlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIle 56
Db 14 CAACAACAACAGCAGCAACTTAAGTCTACTCTCAAAATAAAAGAATGCCATACT 73
QY 57 AspAspTyrLysValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGln 76
Db 74 GATGACTACAAAGTCACTAATCAGGTCTTTGGGACTGGGATCAACGGGAAGGTGCTAGAG 133
QY 77 IlePheAsnLysArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLys 96
Db 134 ATCTTCAGTAAGAAGTCTGGAGAGAAAGTTTCGCTATGAAGATGTTACAGGACTGTGCAAAG 193
QY 97 AlaArgArgGluValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIle 116
Db 194 GCACGCAGGGAGGTAGAACTGCACTGGCGGCTTCCAGTGTCTCATATCGTGAAGATT 253
QY 117 ValAspValTyrGluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCys 136
Db 254 ATTGATGTGTACGAAATCTATACCAGTCTAGAAAGTGTCTTCTTATTATGGAATGT 313
QY 137 LeuAspGlyGlyGluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGlu 156
Db 314 CTGGATGGAGGAGAACTCTTCAGCAGAAATCCAGGATAGAGGGACCAAGCTTTCACGGAG 373
QY 157 ArgGluAlaSerGluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIle 176
Db 374 AGGGAGGCATCTGAGATCATGAGAAGCATTTGGAGAAGCAATCCAGTACTTACACTCTATC 433
QY 177 AsnIleAlaHisArgAspValLysProGluAsnLeuTyrThrSerLysArgProAsn 196
Db 434 AATATTGCCCATAGAGATGTAAAGCCAGAAAATCTCCTATATACATCGAAACGGCCAAAC 493
QY 197 AlaIleLeuLysLeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeu 216
Db 494 TCAGTGTAAAGCTGACTGATTTTGGTTTTGCTAAGGAAACCACATCACACAATTCACATA 553
QY 217 ThrThrProCysTyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyr 236
Db 554 GCAACACCTTGTTTACACACCTTATTATGTTGCTCCTGAAAGTTCTCGGGCCAGAAAATAT 613
QY 237 AspLysSerCysAspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyr 256
Db 614 GACAAGTCGTGTGATATGTGGTCTCTAGGTGTTATCATGTACATTTCTACTATGTGGCTAT 673
QY 257 ProProPheTyrSerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArg 276
Db 674 CCACCATTTTACTCCAACCATGGTTTTCGTCATTTCCCTTGGAAATGAAAAACGAATCCGC 733
QY 277 MetGlyGlnTyrGluPheProAsnProGluTrpSerGluValSerGluGluValLysMet 296
Db 734 ATGGGCCAGTATGAATTTCCAAACCCAGAGTGGTCTGAAGTTTCAGATGAAGTANAACAG 793
QY 297 LeuIleArgAsnLeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMet 316
Db 794 TTGATCAGAAATCTTTGAAGACTGAGCCAACTCAGAGGATGACGATCACAGAATTATG 853
QY 317 AsnHisProTrpIleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArg 336

Db 854 AACCATCCTTTGGATACGCAGTCTATGCAGATTCACC-ACACCTCTTCATACTAGCAGG 912
QY 337 ValLeu 338
Db 913 GTCTTG 918
RESULT 9
AY403347 1149 bp DNA linear GSS 15-DEC-2003
LOCUS Homo sapiens MAPKAPK3 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY403347
VERSION AY403347.1 GI:39759330
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1149)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1149)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source 1..1149
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>1149
/gene="MAPKAPK3"
/locus_tag="HCM1527"
ORIGIN
Alignment Scores:
Pred. No.: 2.92e-109 Length: 1149
Score: 1391.00 Matches: 265
Percent Similarity: 80.2% Conservative: 50
Best Local Similarity: 67.4% Mismatches: 56
Query Match: 66.0% Indels: 22
DB: 14 Gaps: 3
US-10-469-221-2 (1-396) x AY403347 (1-1149)
QY 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProGlnProPro 20
Db 16 GCAGAGGAGCAGGGGGCCCTGTGCC-----CCGCCAGTTGCACCCGGC 60
QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
Db 61 GGACCCGGCTTGGCGGTGTCTCCGGGGGGCGGGGAGCCC----- 102
QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspTyrLys 60
Db 103 -----AAGAAGTACGCACTGACCGACTACCAG 132
QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 133 TTGTCCAAAGCAGGTGTGGCCTGGGTGTGAACGGCAAAGTCTGGAGTCTTCATCGG 192

QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaAArgArgGlu 100
Db 193 CGCACTGGACAGAAGTGTGCCCTGAAGTCTCTGTATGACAGCCCCAAGGCCCGGCAGGAG 252

QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 253 GTAGACCATCACTGGCAGGCTTCTGGCGGCCCCCATATTGTCTGCATCTCGATGTGTAT 312

QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 313 GAGAACATGCACCATGGCAAGCGCTGTCTCTCATCATCATGGAATGCATGGAAGGTGGT 372

QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluAArgGluAlaSer 160
Db 373 GAGTTGTTACGACGAGATTTCAGGAGCGGTGGCGACCAAGCTTTTCACTGAGAGAGAAGCTGCA 432

QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 433 GAGATAATGCGGATATTGGCACTGGCACTGCCATCCAGTTTCTGCACAGCCATAACATTGCCAC 492

QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 493 CGAGATGTCAAGCCTGAAACCTACTCTACACATCTAAGGAGAAAGACGCAGTGCTTAAG 552

QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 553 CTCACCGATTTTGGCTTTGCTAAGGAGACCACC--CAAAATGCCCTGCAGACACCCCTGC 609

QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 610 TATACTCCCTATTATGTGGCCCCCTGAGGTCTGGGTCCAGAGAAGTATGACAAGTCATGT 669

QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 670 GACATGTGGTCCCTGGGTGTTCATCATGTACATCCTCTCTTTGTGGCTTCCCACCCCTTCTAC 729

QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 730 TCCAACACGGGCCAGGCCCATCTCCCCGGGGATGAAGAGGAGGATTCCGCTGGGCCAGTAC 789

QY 281 GlupheProAsnProGluTrpSerGluValSerGluValLysMetLeuIleArgAsn 300
Db 790 GGCTTCCCCCAATCCTGAGTGGTGCAGAAGTCTCTGAGGATGCCAAGCAGCTGATCCGCCTC 849

QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 850 CTGTTGAAGACAGACCCACAGAGAGGCTGACCATCACTCAGTTTCATGAACCAACCCCTGG 909

QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 910 ATCAACCAATCGATGGTAGTGTGCCACAGACCCCACTCCACACGGCCCGAGTGTGCAGGAG 969

QY 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360
Db 970 GACAAAGACCACCTGGGACGAAGTCAAGGAGGAGATGACCAGTGCCCTTGGCCACTATGCGG 1029

QY 361 ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeu 380
Db 1030 GTAGACTACGACCAAGGTGAAGATCAAGGACCTGAAGACCTCTAAACAACCGGCTCCTCAAC 1089

QY 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaAla 393
Db 1090 AAGAGGAGAAAAAAGCAGGCAGGCAGCTCTCTCGCCTCA 1128

RESULT 10
LOCUS CR606251 1799 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DI054YL13 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR606251
VERSION CR606251.1 GI:50487058
KEYWORDS HTC; CNSLT_cDNA.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1799)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
REFERENCE 2 (bases 1 to 1799)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
source
1..1799
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI054YL13"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:
Pred. No.: 5.29e-109 Length: 1799
Score: 1391.00 Matches: 265
Percent Similarity: 80.2% Conservative: 50
Best Local Similarity: 67.4% Mismatches: 56
Query Match: 66.0% Indels: 22
DB: 6 Gaps: 3

US-10-469-221-2 (1-396) x CR606251 (1-1799)

QY 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20
Db 126 GCAGAGGAGCAGGGGGCCCTGTGCC-----CGCCAGTTGCACCCGGC 170

QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
Db 171 GGACCCCGCTTGGCGGTGCTCCGGGGGGGGCGGGAGCCC----- 212

QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspTyrLys 60
Db 213 -----AAGAAGTACGCAGTGACCGACGACTACCAG 242

QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 243 TTGTCCAAGCAGGTGCTGGGCCCTGGGTGTGAACGGCAAAGTCTGGAGTCTTCCATCGG 302

QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaAArgArgGlu 100
Db 303 CGCACTGGACAGAAGTGTCCCTGAAGCTCCTGTATGACAGCCCCAAGGCCCGCAGGAG 362

QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 363 GTAGACCATCACTGGCAGGCTTCTGGCGGCCCCCATATTGTCTGATCTCGATGTGTAT 422

QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 423 GAGAACATGCACCATGGCAAGCGCTGTCTCTCATCATCATGGAATGCATGGAAGGTGGT 482

QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 141

Db	699	-----AAGAACTACGCAGTGACCGACGACTACCAGTTGTGTCCAAAGCAGGTGCTGGGCCTG	752
QY	69	GlyIleAsnGlyLysValLeuGlnIlePheAsnLysArgThrGlnGluLysPheAlaLeu	88
Db	753	GGTGTGAACGCAAAAGTGCTGGAGTGCTTCATCGGGCACTGGACAGAAAGTGTGCCCTG	812
QY	89	LysMetLeuGlnAspCysProLysAlaArgArgGluValGluLeuHisTrpArgAlaSer	108
Db	813	AAGCTCCTGTATGACAGCCCCAAGGCCCGCAGGAGGTAGACCATCACTGGCAGGCTTCT	872
QY	109	GlnCysProHisIleValArgileValAspValTyrGluAsnLeuTyrAlaGlyArgLys	128
Db	873	GGCGGCCCCCATATGTCTGCATCCTGGATGTGTATGAGAACATGCACCATGGCAAGCGC	932
QY	129	CysLeuLeuIleValMetGluCysLeuAspGlyGlyGluLeuPheSerArgIleGlnAsp	148
Db	933	TGTCCTCATCATGATGAATGCATGGAAGGTGGTGAGTTGTTTCAGCAGGATTCAGGAG	992
QY	149	ArgGlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMetLysSerIleGlyGlu	168
Db	993	CGTGGCAGCCAGGCTTTCACCTGAGAGAGAAGCTGCAGAGATAATGCGGGATATTGGCACT	1052
QY	169	AlaIleGlnTyrLeuHisSerIleAsnIleAlaHisArgAspValLysProGluAsnLeu	188
Db	1053	GCCATCCAGTTTCTGCACAGCCATAACATTGCCACCAGAGATGTCAAGCCTGAAACCTA	1112
QY	189	LeuTyrThrSerLysArgProAsnAlaIleLeuLysLeuThrAspPheAlaLys	208
Db	1113	CTCTACACATCTAAGGAGAAAGACGCGAGTGCTTAAGCTCACCGATTGTGGCTTTGCTAAG	1172
QY	209	GluThrThrSerHisAsnSerLeuThrProCysTyrThrProTyrTyrValAlaPro	228
Db	1173	GAGACCACC---CAAAATGCCCTGCAGACACCCCTGCTATACTCCCTATTATGTGGCCCT	1229
QY	229	GluValLeuGlyProGluLysTyrAspLysSerCysAspMetTrpSerLeuGlyValIle	248
Db	1230	GAGGTCCTGGGTCCAGAGAAGTATGACAAGTCATGTGACATGTGGTCCCTGGGTGTCA	1289
QY	249	MetTyrIleLeuLeuCysGlyTyrProPheTyrSerAsnHisGlyLeuAlaIleSer	268
Db	1290	ATGTACATCCTCTTGTGGCTTCCCACCCCTCTACTCCAACACGGGCCAGGCCATCTCC	1349
QY	269	ProGlyMetLysThrArgIleArgMetGlyGlnTyrGluPheProAsnProGluTrpSer	288
Db	1350	CCGGGGATGAAGAGGAGGATTGCGCTGGGGCCAGTACGGCTTCCCCCAATCCTGAGTGTCA	1409
QY	289	GluValSerGluGluValLysMetLeuIleArgAsnLeuLeuLysThrGluProThrGln	308
Db	1410	GAAGTCTCTGAGGATGCCAAGCAGCTGATCCGCTCTCTGTTGAAGACAGACCCACAGAG	1469
QY	309	ArgMetThrIleThrGluPheMetAsnHisProTrpIleMetGlnSerThrLysValPro	328
Db	1470	AGGCTGACCATCACTCAGTTCATGAACCAACCCCTGGATCAACCAATCGATGGTAGTGCCA	1529
QY	329	GlnThrProLeuHisThrSerArgValLeuLysGluAspLysGluArgTrpGluAspVal	348
Db	1530	CAGACCCCACTCCACACGCCCCGAGTGTGCAGGAGGACAAAGACCACCTGGGACGAAGTC	1589
QY	349	LysGluGluMetThrSerAlaLeuAlaThrMetArgValAspTyrGluGlnIleLysIle	368
Db	1590	AAGGAGGAGATGACCACTGCTTGGCCACTATGCGGGTAGACTACGACCAGGTGAAGATC	1649
QY	369	LysLysIleGluAspAlaSerAsnProLeuLeuLysArgArgLysLysAlaArgAla	388
Db	1650	AAGGACCTGAAGACCTCTAACACCCGGCTCCTCAACAGAGGAGAGAAAAAGCAGGCAGGC	1709
QY	389	LeuGluAlaAlaAla 393	
Db	1710	AGCTCCTCTGCCTCA 1724	
RESULT 12			
AY403349			
LOCUS			
AY403349 1155 bp DNA linear GSS 15-DEC-2003			

DEFINITION	Mus musculus MAPKAPK3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.		
ACCESSION	AY403349		
VERSION	AY403349.1 GI:39759332		
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.		
	1 (bases 1 to 1155)		
	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCE	2 (bases 1 to 1155)		
	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
	Direct Submission		
	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
FEATURES	Location/Qualifiers		
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ORIGIN	/locus_tag="HCM1527"		
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QY	Percent Similarity:	80.7%	Conservative: 51
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	Query Match:	64.6%	Indels: 26
	DB:	14	Gaps: 3
US-10-469-221-2 (1-396) x AY403349 (1-1155)			
QY	19	ProProThrProAlaLeu-----ProHisProProAlaGln	30
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QY	31	ProProProProGlnGlnPheProGlnPheHisValLysSerGlyLeuGlnIle	50
Db	100	CGGGAACCC-----	108
QY	51	LysLysAsnAlaIleIleAspAspTyrLysValThrSerGlnValLeuGlyLeuGlyIle	70
Db	109	AAGAAGTACGCGGTGACTGATGACTACCAAGCAAGTGTGGGTCTGGGTGTG	168
QY	71	AsnGlyLysValLeuGlnIlePheAsnLysArgThrGlnGluLysPheAlaLeuLysMet	90
Db	169	AACGGCAAGGTACTGGAGTGCTACCATCGGCGCTCTGGCCAGAAAGTGTGCCCTGAAGCTC	228
QY	91	LeuGlnAspCysProLysAlaArgArgGluValGluLeuHisTrpArgAlaSerGlnCys	110
Db	229	CTGTATGACAGCCCCCAAGGCCCGCAGGAGGTGGACCACTGGCAGGCGTCAAGCGGC	288
QY	111	ProHisIleValArgIleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCysLeu	130
Db	289	CCCCACATCGTGGCGCATCCTGGACGTGTATGAGAATATGCACCACGGCAGCGCTCTC	348

Qy	131	LeuIleValMetGluCysLeuAspGlyGlyGluLeuPheSerArgIleGlnAspArgGly	150
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Qy	151	AspGlnAlaPheThrGluArgGluAlaSerGluIleMetLysSerIleGlyGluAlaIle	170
Db	409	GACCAGGCTTTCACTGAGAGAGAGGCTGCAGAGATAATGCGGACATTGGCACTGCCATC	468
Qy	171	GlnTyrLeuHisSerIleAsnIleAlaHisArgAspValLysProGluAsnLeuLeuTyr	190
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Qy	191	ThrSerLysArgProAsnAlaIleLeuLysLeuThrAspPheGlyPheAlaLysGluThr	210
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Qy	211	ThrSerHisAsnSerLeuThrThrProCysTyrThrProTyrTyrValAlaProGluVal	230
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Qy	231	LeuGlyProGluLysTyrAspLysSerCysAspMetTrpSerLeuGlyValIleMetTyr	250
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Qy	251	IleLeuLeuCysGlyTyrProProPheTyrSerAsnHisGlyLeuAlaIleSerProGly	270
Db	706	ATCCTTTTGTGTGGATTCCCAACCCTTCTACTCCAACCCGCGCAGGCCATCTCTCCAGGA	765
Qy	271	MetLysThrArgIleArgMetGlyGlnTyrGluPheProAsnProGluTrpSerGluVal	290
Db	766	ATGAAAAGAAGGATTTCGCTTGGGCCAGTATAGCTTCCCTAACCTGAATGGTTAGATGTC	825
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Db	826	TCTGAGGATGCCAAGCAGCTAATCCGCTGCTCTGAAGACAGATCCCAAGAGAGGCTA	885
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Qy	351	GluMetThrSerAlaLeuAlaThrMetArgValAspTyrGluGlnIleLysIleLysLys	370
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Db	1126	TCAGCCTCA	1134
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LOCUS			
DEFINITION			
AK087496 2481 bp mRNA linear HTC 02-SEP-2005			
Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130306K23 product:Similar to mitogen-activated protein kinase-activated protein kinase 3, full insert sequence.			
AK087496			
ACCESSION			
AK087496.1 GI:26352533			
HTC; CAP trapper.			
KEYWORDS			
Mus musculus (house mouse)			
SOURCE			
ORGANISM			
Mus musculus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.			
1			
REFERENCE			
Carninci, P. and Hayashizaki, Y.			
High-efficiency full-length cDNA cloning			

JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	5
AUTHORS	The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6
AUTHORS	RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium.
TITLE	Antisense Transcription in the Mammalian Transcriptome
JOURNAL	Science 309, 1564-1566 (2005)
REFERENCE	7
AUTHORS	The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).
TITLE	The Transcriptional Landscape of the Mammalian Genome
JOURNAL	Science 309, 1559-1563 (2005)
REFERENCE	8 (bases 1 to 2481)
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	
Please visit our web site for further details.	
URL:http://genome.gsc.riken.jp/	
URL:http://fantom.gsc.riken.jp/	
Location/Qualifiers	
1. .2481	
FEATURES	
source	


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ORIGIN

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Alignment Scores:
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Best Local Similarity: 64.7%    Mismatches:   54
Query Match:      64.6%        Indels:       38
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US-10-469-221-2 (1-396) x AK087496 (1-2481)

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QY      22 ProAlaLeuProHisProProAla-----GlnProProPro----- 33
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QY      34 -----ProProProGlnGlnPheProGlnPheHisVal 44
Db      121 CTCGGGGGGTCCGCCTTGGGTGGTGTCTCCGGCCCCA----- 156

QY      45 LysSerGlyLeu-----GlnIleLysLysAsnAlaIleAspAspTyrLysValThr 62
Db      157 -----GGTGTGCGACGGGAACCCCAAGAGTACGCGGTGACTGACTACTACCGATTGTCC 210

QY      63 SerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLysArgThr 82
Db      211 AAGCAAGTGTGGGTCTGGGTGTGAACGGCAAGGTACTGGAGTGTCTACCATCGGCGCTCT 270

QY      83 GlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGluValGlu 102
Db      271 GGCCAGAAGTGTGCCCTGAAGTCTCTGTATGACAGCCCCCAAGGCCCGGAGGAGGTGGAC 330

QY      103 LeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyrGluAsn 122
Db      331 CACCACCTGGCAGCGCTCAGCGGCCCCCACATCTGTGGCATCTCTGGACGTATGAGAAT 390

QY      123 LeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGlyGluLeu 142
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QY      183 ValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLysLeuThr 202
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QY      303 LysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrpIleMet 322
Db      928 AAGACAGATCCACAGAGAGGCTAACGATCATGCAGTTTATGAACCATCCTTGGATCAAT 987

QY      323 GlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGluAspLys 342
Db      988 CAATCCATGGTGGTCCCACAGACCCCACTCTACACAGCCCGAGTGTCTCCAGGAAGACAAA 1047

QY      343 GluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArgValAsp 362
Db      1048 GATCACTGGGATGACGTCGAAGGAAGAGATGACCAAGTGCCTGGCCACTATCGGGTAGAC 1107

QY      363 TyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLysArg 382
Db      1108 TATGACCAGGTGAAGATCAAGGACCTGAAGACCTCTAACAAACCGGCTCCTCAACAAGAGG 1167

QY      383 ArgLysLysAlaArgAlaLeuGluAlaAlaAla 393
Db      1168 AGGAAAAAGCAGGCAGGCAGCTCCTCAGCCTCA 1200

RESULT 14
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LOCUS
DEFINITION
AKI72344
2724 bp mRNA linear HTC 21-SEP-2005
Mus musculus activated spleen cDNA, RIKEN full-length enriched
library, clone:F830203H07 product:Similar to mitogen-activated
protein kinase-activated protein kinase 3, full insert sequence.
AKI72344
AKI72344.1 GI:74186376
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
2
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
```

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159

3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861

4
Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,

Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
and Hayashizaki,Y.

RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
11217851

5
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
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Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasaki,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Perteaux,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Sandelin,A., Schneider,C., Sempke,C.A., Setou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
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Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.

FANTOM Consortium
TITLE
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

JOURNAL
PUBMED
REFERENCE
AUTHORS

Nature 420 (6915), 563-573 (2002)
12466851

6
Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C.,
Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R.,
Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R.,
Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E.,
Ambesi-Impombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L.,
Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M.,
Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R.,
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di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G.,
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Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E.,
Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N.,
Hill,D., Humnietki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T.,
Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H.,
Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K.,
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Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L.,
Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S.,
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Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavese,G.,
Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z.,
Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A.,
Schneider,C., Schonbach,C., Sekiguchi,K., Sempke,C.A., Seno,S.,
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Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R.,
Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R.,
Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A.,
Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,B.T.,
Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A.,
Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M.,
Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M.,
Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M.,
Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M.,
Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K.,
Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
FANTOM Consortium
TITLE
The transcriptional landscape of the mammalian genome
Science 309 (5740), 1559-1563 (2005)
16141072

7
Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M.,
Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H.,
Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T.,
Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L.,
Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A.,
Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and
Wahlestedt,C.
RIKEN Genome Exploration Research Group
TITLE
Antisense transcription in the mammalian transcriptome
Science 309 (5740), 1564-1566 (2005)
16141073

8 (bases 1 to 2724)
Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K.,
Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S.,
Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N.,
Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D.,
Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken

CONSRM
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

The transcriptional landscape of the mammalian genome
Science 309 (5740), 1559-1563 (2005)
16141072

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Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M.,
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Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A.,
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Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N.,
Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D.,
Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission

Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken

COMMENT

COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane,Q 4072 Australia) whose assistance we gratefully acknowledge. please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/ Location/Qualifiers		
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CDS			
Alignment Scores:			
Pred. No.:	3.54e-106	Length:	2732
Score:	1361.00	Matches:	258
Percent Similarity:	80.7%	Conservative:	51
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US-10-469-221-2 (1-396) x AK151881 (1-2732)			
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QY	51	LysLysAsnAlaIleIleAspAspTyrLysValThrSerGlnValLeuGlyLeuGlyIle	70
Db	437	AAGAAGTACGCGGTGACTGATGACTACCACTGTTGCCAAGCAAGTGTGGGTCTGGGTGTG	496
QY	71	AsnGlyLysValLeuGlnIlePheAsnLysArgThrGlnGluLysPheAlaLeuLysMet	90
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QY	91	LeuGlnAspCysProLysAlaArgArgGluValGluLeuHisTyrArgAlaSerGlnCys	110
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Search completed: June 19, 2006, 17:01:44
Job time : 6145 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 19, 2006, 14:41:57 ; Search time 815 Seconds
(without alignments)
5081.614 Million cell updates/sec

Title: US-10-469-221-2
Perfect score: 2106
Sequence: 1 SQGQSPVPFPAPAPPPQPP.....PLLLKRRKKARALEAAALAH 396

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abss/ABSSEWEB spool/US10469221/runat_19062006_062546_959/app_query.fasta_1
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description

1	2106	100.0	1191 8	Aad50036 Human tru
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3	2097	99.6	1203 14	Adv43403 Human psy

4	2097	99.6	1726	12	ADM36339	Adm36339 Human MK2
5	2097	99.6	1726	14	ADX06659	Adx06659 Cyclin-de
6	2078	98.7	1336	6	ABK84657	Abk84657 Human CDN
7	2078	98.7	1336	11	ADI32071	Adi32071 Human CDN
8	2078	98.7	1336	13	ADS84138	Ads84138 Human lym
9	2006.5	95.3	2263	6	ABV73995	Abv73995 Human MAP
10	2006.5	95.3	2263	9	ACA62272	ACA62272 Human DNA
11	2006.5	95.3	2263	12	ADM36337	Adm36337 Human MK2
12	2006.5	95.3	2263	14	ADX06657	Adx06657 Cyclin-de
13	2006.5	95.3	2263	14	ADY86797	Ady86797 Human MAP
14	2006.5	95.3	2263	14	AEA89439	Aea89439 Human MAP
15	2006.5	95.3	3608	14	ADZ49304	Adz49304 Insulin s
16	1991.5	94.6	2258	6	ABL67227	Abi67227 Thyroid c
17	1991.5	94.6	2258	10	ACA56817	Aca56817 Human sig
18	1991.5	94.6	2258	12	ADI56613	Adi56613 Human pol
19	1991.5	94.6	2258	12	ADP87578	Adp87578 Human NOV
20	1991.5	94.6	2258	14	AED17914	Aed17914 Fibrotic
21	1925.5	91.4	2802	3	AAF15803	Aaf15803 Human pro
22	1886	89.6	2592	13	ACN41322	Acn41322 Human dia
23	1882	89.4	1113	14	ADV43402	Adv43402 Human psy
24	1882	89.4	1128	12	ADP87584	Adp87584 Human NOV
25	1870	88.8	1130	12	ADP87582	Adp87582 Human NOV
26	1870	88.8	1133	12	ADP87586	Adp87586 Human NOV
27	1803	85.6	1026	12	ADP87588	Adp87588 Human NOV
28	1729	82.1	1305	9	ACF57389	Acc57389 SUMO-MPAK
29	1720.5	81.7	3186	8	ACC46238	Acc46238 Human dit
30	1716	81.5	981	12	ADN61587	Adn61587 DNA encod
31	1709	81.1	1168	14	AEI13869	Aee13869 Hamster c
32	1552	73.7	885	12	ADP87580	Adp87580 Human NOV
33	1552	73.7	885	12	ADP87590	Adp87590 Human NOV
34	1391	66.0	1149	14	AEI19658	Aee19658 Human MAP
35	1391	66.0	1298	6	ABK84332	Abk84332 Human CDN
36	1391	66.0	2481	6	ABK84214	Abk84214 Human CDN
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39	1391	66.0	2481	10	ACA56490	Aca56490 Human sig
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43	1391	66.0	2500	12	ADQ87216	Adq87216 Human tum
44	1391	66.0	2500	15	AEF92766	Aef92766 Human mit
45	1391	66.0	2509	11	ADN95702	Adn95702 Human BEC

ALIGNMENTS

RESULT 1
AAD50036
ID AAD50036 standard; cDNA; 1191 BP.

XX
AC AAD50036;

XX
DT 24-MAR-2003 (first entry)

XX
DE Human truncated MAPKAP-2 kinase, tdnMAPKAP-2 cDNA.

XX
KW Human; mitogen-activated protein kinase activating protein kinase-2;
KW MAPKAP-2 kinase; signal transduction; cell proliferative disorder;
KW immune system disorder; inflammation; arthritis; immunomodulator;
KW cytostatic; gene therapy; enzyme; gene; ss.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers

FT CDS 1..1191
FT /*tag= a
FT /product= "Human tdnMAPKAP-2"
FT /note= "No start codon"
FT /partial

XX
PN WO200290524-A2.

XX
PD 14-NOV-2002.

XX 14-NOV-2002.
PD
XX
PF 25-FEB-2002; 2002WO-US005670.
XX
PR 28-FEB-2001; 2001US-0272260P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Lograsso P, Hawkins J, Lisnock JM;
XX
DR WPI; 2003-111970/10.
DR P-PSDB; AAE29899.
XX
PT New isolated nucleic acid molecule encoding a human mitogen-activated
PT protein kinase activating protein kinase-2 (MAPKAP-2), useful for
PT treating immune-system related disorders, inflammation and arthritis.
XX
PS Claim 63; Fig 3; 150pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule comprising a
CC sequence of nucleotides that encode a human mitogen-activated protein
CC kinase activating protein kinase-2 (MAPKAP-2 kinase) and a coding region
CC that encodes a splice variant of a MAPKAP-2 kinase. The invention is
CC especially useful in regulating signal transduction in a cell and in
CC diagnosing or treating MAPKAP-2-mediated disorders eg. cell proliferative
CC disorders, immune system disorders, inflammation, arthritis. The nucleic
CC acid and the polypeptide may also be used in screening assays, predictive
CC medicine, diagnostic or prognostic assays, chromosome mapping, tissue
CC typing, pharmacogenomics and in monitoring clinical trials. The invention
CC is useful in gene therapy. The present sequence is human full length
CC MAPKAP-2 kinase, fldnaMAPKAP-2 cDNA
XX
SQ Sequence 1203 BP; 303 A; 366 C; 313 G; 221 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.55e-141 Length: 1203
Score: 2106.00 Matches: 396
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Dbs: 8 Gaps: 0

US-10-469-221-2 (1-396) x AAD50037 (1-1203)

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Dbs 13 TCCAGGGCCAGAGCCCGGTGCGTTCCTCCCGCCCGCCCGCCCGCCCGCCCGCC 72

QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProProProGlnGlnPhePro 40
Dbs 73 ACCCTGCCCCCTGCCGCACCCCGCGCGCAGCCCGCCCGCCCGCCCGCCCGCCCG 132

QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspAspTyrLys 60
Dbs 133 CAGTCCACGTCAGTCCGGCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 192

QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Dbs 193 GTCACAGCCAGGTCCTCGGGCTGGGCATCAACGGCAAAGTTTTCAGATCTTCAACAAG 252

QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Dbs 253 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGCCCGCAGGGAG 312

QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Dbs 313 GTGGAGCTGCACCTGGCGGGCCCTCCAGTGCCTCCGCACATCGTACGGATCGTGGATGTGTAC 372

QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Dbs 373 GAGAATCTGTACGCAGGGAGGAAGTGCCTGCTGATTGTCATGGAAATGTTTGGACGGTGA 432

QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Dbs 433 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACGAGCATTCACAGAAAGAGAGCATCC 492

QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Dbs 493 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATGCCCCAT 552

QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Dbs 553 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCTCTGAAA 612

QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Dbs 613 CTCACGTGACTTTGGCTTTGCCAAGGAAACCCACGAGCCACAACCTCTTTGACCACTCCTGT 672

QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Dbs 673 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAGTATGACAAGTCCTGT 732

QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProPheTyr 260
Dbs 733 GACATGTGGTCCCTGGGTGTTCATCATGTACATCTGCTGTGTGGGTATCCCCCTCTCTAC 792

QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Dbs 793 TCCAACCCAGCCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 852

QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Dbs 853 GAATTTCCCAACCCAGAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 912

QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Dbs 913 CTGCTGAAAACAGAGCCCAACCCAGAGAATGACCATCACCGAGTTTATGAACCCCTTGG 972

QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Dbs 973 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCCGCGGTCTCTGAAGGAG 1032

QY 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360
Dbs 1033 GACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCATGCTTGGCCACAATGCGC 1092

QY 361 ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeu 380
Dbs 1093 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACCCCTCTGCTGCTG 1152

QY 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaAlaLeuAlaHis 396
Dbs 1153 AAGAGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCCAC 1200

RESULT 3
ADV43403
ID ADV43403 standard; cDNA; 1203 BP.
XX
AC ADV43403;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1031.
XX
KW microarray; psychoneuroendocrinimmune; chronic fatigue;
KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO2004108899-A2.
XX
PD 16-DEC-2004.
XX
PF 04-JUN-2004; 2004WO-US017686.

XX 04-JUN-2003; 2003US-0475915P.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Nicholson A, Vernon SD;
XX WPI; 2005-031682/03.
DR
XX New microarray comprising probes for genes involved in
PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
XX
PS Claim 1; SEQ ID NO 1031; 254pp; English.
XX
CC The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI
CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC cancer and infection. The present sequence represents a
CC psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC SEQ ID NO 1829 are provided.
XX
SQ Sequence 1203 BP; 303 A; 365 C; 313 G; 222 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.83e-141 Length: 1203
Score: 2097.00 Matches: 395
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.6% Indels: 0
DB: 14 Gaps: 0

US-10-469-221-2 (1-396) x ADV43403 (1-1203)

QY 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20
Db 13 TCCAGGGCCAGACCCCGCGGTGCCGTCCTCCCGCCCGCCCGCCGCGAGCCCCC 72

QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProProGlnGlnPhePro 40
Db 73 ACCCTGTCCTGCGCACCCCGCGCGAGCGCGCCCGCCCGCCCGCGAGCAGTTCCCG 132

QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleAspTyrLys 60
Db 133 CAGTTCACGTCAGTCGGCCTGCAGATCAAGAAGAAGACGCCATCATCGATGACTACAAG 192

QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 193 GTCACCAGCCAGGTCTCTGGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAG 252

QY 81 ArgThrGlnGlnLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Db 253 AGGACCCAGGAGAAATTGCCCCCTCAAAATGCTTCAGGACTGCCCCCAAGGCCCGCAGGGAG 312

QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 313 GTGGAGCTGCATCGCGGGCCCTCCCAAGTGCCCCGACATCGTACGGATCGTGGATGTGTAC 372

QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 373 GAGAAATCTGTACGAGGGGAGGAAGTGCCCTGCTGATTGTTCATGGAATGTTGGACGGTGA 432

QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 433 GAACCTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAGAAGAGCATCC 492

QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 493 GAAATCATGAAGAGCATCGGTGAGGCCCATCCAGTATCTGCATTTCATCAATCAACATTGCCCAT 552

QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 553 CGGGATGTCAAGCCTGAGAATCTTTATACACCTCCAAAGGCCCAACGCCATCCTGAAA 612

QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 613 CTCACGTACTTTGGCTTTGCCAAGGAAACACCAGCCACAACCTCTTTGACCACCTCCTGT 672

QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 673 TATACACCGTACTATGTGGCTCCAGAAGTGTGGGTCCAGAGAAGTATGACAAGTCCTGT 732

QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProPropheTyr 260
Db 733 GACATGTGGTCCCTGGGTGTCATCATGTACATTTCTGTGTGGGTATCCCCCTTCTAC 792

QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 793 TCCAACACACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 852

QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 853 GAATTTCCCAACCCAGAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 912

QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 913 CTGCTGAAAAACAGAGCCCCACCCAGAGAATGACCATCACCCGAGTTTATGAACCCCTTGG 972

QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 973 ATCATGCAATCAACAAAGGTCCTCAAAACCCACTGCACACCCAGCCGGTCTCTGAAGGAG 1032

QY 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360
Db 1033 GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAGTGCCTTGGCCACAATGCGC 1092

QY 361 ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeu 380
Db 1093 GTTACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACCCCTCTGTGCTGT 1152

QY 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 1153 AAGAGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGSGCCAC 1200

RESULT 4
ADM36339
ID ADM36339 standard; cDNA; 1726 BP.
XX
AC ADM36339;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human MK2 variant 2 encoding cDNA SEQ ID NO:3.
KW ischaemic injury;
KW mitogen-activated protein kinase-activated protein kinase 2; MK2;
KW vasotropic; cerebroprotective; cardiant; hypotensive;
KW antiarteriosclerotic; thrombolytic; neuroprotective; cardiovascular;
KW antiangular; antiarrhythmic; MK2 antagonist; cerebral ischaemia;
KW ischaemia; vascular occlusion; cerebral infarction; stroke;
KW cerebral vascular disease; myocardial infarction;
KW coronary artery disease; congestive heart failure; cardiac arrhythmia;
KW unstable angina; high blood pressure; claudication;
KW peripheral occlusive arterial disease; atherosclerosis;
KW thrombotic condition; thromboembolic condition; CNS disorder; human;
KW MK2 variant 2; chromosome 1q32; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 379..1581
FT /*tag= a
FT /product= "MK2 variant 2"

KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
XX WO200228999-A2.
PN
XX
XX 11-APR-2002.
PD
XX
XX 03-OCT-2001; 2001WO-US030821.
PF
XX
XX 03-OCT-2000; 2000US-0237189P.
PR
XX
XX (GENE-) GENE LOGIC INC.
PA
XX
XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
PI
XX
XX WPI; 2002-435328/46.
DR
XX
XX

PT Detecting granulocyte activation by detecting differential expression of
PT genes associated with granulocyte activation, which serves as diagnostic
PT markers that is useful for monitoring disease states and drug toxicity.
XX
XX
PS Claim 1; SEQ ID NO 1228; 114pp; English.

CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing the
CC expression level to an expression level in an unactivated GC, where
CC differential expression of Gs is indicative of GCA. Also included are
CC modulating (M2) GA by contacting GC with an agent that alters the
CC expression of at least one gene in Gs; (2) screening (M3) for an agent
CC capable of modulating GCA or an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease using the gene expression
CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease, by detecting the level of
CC expression in a sample of the tissue of gene(s) from Gs, where the level
CC of expression of the gene is indicative of inflammation; (4) treating
CC (M5) an inflammation (especially chronic) or in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease, by contacting a tissue having inflammation with an
CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
CC is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful
CC for screening an agent capable of modulating GCA preferably in an
CC inflammation in a tissue; M4 is useful for detecting an inflammation
CC (especially chronic) in a tissue, an allergic response in a subject,
CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
CC disease, ulcerative colitis, periodontal disease; also bacterial
CC infection, viral infection, parasitic infection, protozoal infection,
CC fungal infection and M5 is useful for treating one of the above
CC conditions. The present sequence represents a gene differentially
CC expressed in granulocytes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1336 BP; 338 A; 406 C; 340 G; 252 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.75e-139 Length: 1336
Score: 2078.00 Matches: 393
Percent Similarity: 99.2% Conservative: 0

Best Local Similarity: 99.2% Mismatches: 3
Query Match: 98.7% Indels: 0
DB: 6 Gaps: 0

US-10-469-221-2 (1-396) x ABK84657 (1-1336)

QY 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20
Db 1 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCGCCCGCGCCCGCGCAGCCCCC 60

QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
Db 61 ACCCTGCCCTGCCGACCCCCCGCGCAGCGCGCGCGCGCGCGCGAGTTCCCG 120

QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspTyrLys 60
Db 121 CAGTTCACGTCAGTCCGGCTGCAGATCAAGAGAACGCCATCATCGATGACTACAAG 180

QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 181 GTCACGAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTTGCAGATCTTCAACAAG 240

QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu 100
Db 241 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCAAGGCCGAGGAG 300

QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 301 GTGGAGCTGCACGTGGCGGCCCTCCAGTCCCGGACATCGTACGGATCGTGGATGTGTAC 360

QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 361 GAGAAATCTGTACGAGGAGGAAAGTGCCTGCTGATTTGCATGGAATGTTGGACGGTGA 420

QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACGAGGCATTCACAGAAAGAGAGCATCC 480

QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATGCCCCAT 540

QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 541 CGGGATGTCAAGCCTGAGAATCTCTTATACACTCCAAAGGCCCAACGCCATCCTGAAA 600

QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 601 CTCACGTACTTTGGCTTGCCAAGGAAACCAACGAGCCACAACCTCTTTGACCACTCCTGT 660

QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 661 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAAGTATGACAAAGTCTGT 720

QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 721 GACATGTTGGTCTGGGTGTTCATCATGTACATTTCTGTGTGGGTATCCCCCTTCTAC 780

QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 781 TCCAACCCAGCGCTGCCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCCAGTAT 840

QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 841 GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900

QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 901 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACACCCTTGG 960

QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 961 ATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCAGCCGGGTCTTGAAGGAG 1020

Qy	341	AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg	360
Db	1021	GACAAAGGACCGTGGGAGGATGTCAAGGAGGAGATGACCAGTGCCCTTGCCACAATGCGC	1080
Qy	361	ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeu	380
Db	1081	GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAAACCTCTGCTGCTG	1140
Qy	381	LysArgArgLysLysAlaArgAlaLeuGluAlaAlaAlaLeuAlaHis	396
Db	1141	AAGAGGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCCAC	1188

carcinogenicity studies, forensics or pharmacogenomics. The composition may also be used in purification of a subpopulation of mRNAs, cDNAs or genomic fragments. This sequence represents a human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

Alignment Scores:	
pred. No.:	1.75e-139
Score:	2078.00
Percent Similarity:	99.2%
Best Local Similarity:	99.2%
Query Match:	98.7%
DB:	11
	Length:
	Matches:
	Conservative:
	Mismatches:
	Indels:
	Gaps:
	1336
	393
	0
	3
	0
	0

Qy	1	SerGlnGlyGlnSerProProValPropheProAlaProAlaProProProGlnProPro	20
Db	1	TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCTCCCGCCCGCGCCCGCGCCGCGCAGCCCCC	60
Qy	21	ThrProAlaLeuProHisProProAlaGlnProProProProProProGlnGlnPhePro	40
Db	61	ACCCCTGCCCTGCCGACCCCGCGCGCAGCCCGCGCGCGCCCGCGCAGCAGTTCCCG	120
Qy	41	GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspAspTyrLys	60
Db	121	CAGTTCACGTCAAGTCCGGCCTGCAGATCAAGAAAGAACGCCATCATCGATGACTACAAG	180
Qy	61	ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys	80
Db	181	GTCAACCAGCAGGTCTCTGGGCTGGGCATCAACGCGAAAGTTTGCAGATCTTCAACAAG	240
Qy	81	ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu	100
Db	241	AGGACCCAGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCCAAGGCCCGCAGGGAG	300
Qy	101	ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr	120
Db	301	GTGGAGCTGCACTGGCGGGCCTCCCAGTGGCCCGACATCGTACGGATCGTGGATGTGTAC	360
Qy	121	GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly	140
Db	361	GAGAAATCTGTACGCAGGGAGGAAGTGCTGTGATTGTTCATGGAAATGTTTGGACGGTGA	420
Qy	141	GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer	160
Db	421	GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTACAGAAAAGAGAAGCATCC	480
Qy	161	GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis	180
Db	481	GAAATCATGAGAGCATCGGTGAGGCCATCCAGTATCTGCATTTCATCAACATTGCCCAT	540
Qy	181	ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys	200
Db	541	CGGGATGTCAGCCCTGAGAACTCTTTATACACCTCCAAAAGGCCCAACGCCATCTTGAAA	600
Qy	201	LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys	220
Db	601	CTCACTGACTTTGGCTTTGCCAAGGAAACCAACGACCACAACTCTTTTGACCACTCCTTGT	660
Qy	221	TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys	240
Db	661	TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAAGTCTCTGT	720
Qy	241	AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProPropheTyr	260
Db	721	GACATGTTGGTCTCGGTGTTCATCATGTACATTCTGCTGTGTGGGTATCCCCCCTTCTAC	780
Qy	261	SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr	280

Db 781 TCCAAACACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGCCAGTAT 840
QY 281 GluPheProAsnProGluTrpSerGluValSerGluValLysMetLeuIleArgAsn 300
Db 841 GAAATTCCCAACCCAGAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 901 CTGCTGAAAACAGAGCCCAACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCTTGG 960
QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 961 ATCATGCAATCAACAAGGTCCCTCAAACCCCACTGCACACCGCGGTCCTGAAGGAG 1020
QY 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360
Db 1021 GACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACAGTGCCCTTGGCCACAATGCGC 1080
QY 361 ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeu 380
Db 1081 GTTGACTACGAGCAGATCAAGATAAAAAAAGATTGAAGATGCATCCAACCCCTCTGCTGCTG 1140
QY 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 1141 AAGAGGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCCAC 1188

RESULT 8
ADS84138
ID ADS84138 standard; cDNA; 1336 BP.
XX
AC ADS84138;
XX
DT 11-AUG-2005 (first entry)
XX
DE Human lymph node cDNA #1397.
XX
KW ss; gene; human; immunological response; blood cell; cancer;
KW immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;
KW bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
KW osteoporosis; pancreatitis; infection; arthritis; lymph node.
XX

OS Homo sapiens.
XX
PN US2004077003-A1.
XX
PD 22-APR-2004.
XX
PF 14-AUG-2003; 2003US-00641643.
XX
PR 09-FEB-1998; 98US-00023655.
XX
PA (INCY-) INCYTE CORP.
XX
PI Cocks BG, Stuart SG, Seilhamer JJ;
XX
DR WPI; 2004-387937/36.
XX
PT New compositions having a number of first, second and third
PT polynucleotide probes, useful in research and diagnostic applications in
PT cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
PT infections.
XX
PS Claim 15; SEQ ID NO 1397; 16pp; English.
XX
CC The invention relates to polynucleotides which are used as probes to
CC detect genes differentially expressed in an immunological response,
CC abundantly expressed in an immunological response and/or coding for a
CC polypeptide known to regulate blood cell biology. The polynucleotides are
CC useful in research and diagnostic applications particularly in cancer and
CC immunopathological conditions, such as AIDS, allergies, anaemia, asthma,
CC atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
CC sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
CC present sequence represents a human lymph node cDNA used to detect blood

CC cell and immunological response gene expression. Note: The present
CC sequence does not appear in the printed specification but was obtained in
CC electronic format from the USPTO web site.
CC (seqdata.uspto.gov/sequence.html?DocID=20040077003).
XX
SQ Sequence 1336 BP; 338 A; 406 C; 340 G; 252 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.75e-139 Length: 1336
Score: 2078.00 Matches: 393
Percent Similarity: 99.2% Conservative: 0
Best Local Similarity: 99.2% Mismatches: 3
Query Match: 98.7% Indels: 0
DB: 13 Gaps: 0

US-10-469-221-2 (1-396) x ADS84138 (1-1336)

QY 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProGlnProPro 20
Db 1 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCGCCCGCCGAGCCCCC 60
QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
Db 61 ACCCTGCCCTGCCGACCCCCCGGCGAGCGCGCCCGCCCGCCGAGTCCCG 120
QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspTyrLys 60
Db 121 CAGTTCCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 180
QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 181 GTCACCAGCCAGGTCTCGGGCTGGGCATCAACGGCAAAAGTTTTGCAGATCTTCAACAAG 240
QY 81 ArgThrGlnGlyLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Db 241 AGGACCCAGGAGAAATTGCCCTCAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 300
QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 301 GTGAGCTGCACCTGGCGGCCCTCCAGTCCCGGCACATCGTACGGATCGTGGATGTGTAC 360
QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 361 GAGAACTCTGTACGAGGGAGGAAGTGCCTGCTGATTGTCATGGAATGTTTGGACGGTGA 420
QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 421 GAACTCTTTAGCCGAATCCAGGATCGAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGAAGCATCC 480
QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 540
QY 181 ArgAspValLysProGluAsnLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 541 CGGGATGTCAAGCCTGAGAAATCTCTTATACACCTCCAAAGGCCCAACGCCATCCTGAAA 600
QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 601 CTCACTGACTTTGGCTTTGCCAAGGAAACACCAGCCACAACACTCTTTGACCACACTCCTTGT 660
QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 661 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGGTCCAGAGAAAGTATGACAAGTCCTGT 720
QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProPropheTyr 260
Db 721 GACATGTTGGTCTCGGTGTTCATCATGTACATCTGCTGTGTGGGTATCCCCCTTCTAC 780
QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 781 TCCAACCAACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840

QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
|||||
Db 841 GAATTTCACACCCAGAAATGGTCAGAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900

QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
|||||
Db 901 CTGCTGAAAACAGAGCCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGG 960

QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
|||||
Db 961 ATCATGCAATCAACAAAGGTCCTCTCAAAACCCCACTGCACACCAGCCGGTCTCTGAAGGAG 1020

QY 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360
|||||
Db 1021 GACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCATGCGCTTGGCCACAATGCGC 1080

QY 361 ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeu 380
|||||
Db 1081 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCCAACCCCTCTGCTGCTG 1140

QY 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaAlaLeuAlaHis 396
|||||
Db 1141 AAGAGGCGGAAGAAAGCTCGGGCCCTGGAGGCTGGGCTCTGGCCCCAC 1188

RESULT 9
ABV73995
ID ABV73995 standard; cDNA; 2263 BP.
XX
AC ABV73995;
XX
DT 13-JAN-2003 (first entry)
XX
DE Human MAPKAP kinase 2 cDNA.
XX
KW MAPKAP kinase 2; tyrosine threonine kinase; TTK; protein kinase; enzyme;
KW mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;
KW human; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 379..1491
CDS /*tag= a
FT /*product= "MAPKAP kinase 2"
XX
PN WO200268444-A1.
XX
PD 06-SEP-2002.
XX
PF 21-FEB-2002; 2002WO-US005278.
XX
PR 21-FEB-2001; 2001US-0271254P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Reinhard C, Jefferson AB, Chan VW;
XX
XX WPI; 2002-698650/75.
DR P-PSDB; ABP54949.
XX
PT Reducing growth of cancer cells comprises reducing Tyrosine Threonine
PT Kinase (TTK) activity, useful in diagnosing and treating disorders with
PT abnormal expression levels and activity of TTK, such as lung, colon,
PT prostate and ovarian cancer.
XX
PS Disclosure; Page 106-107; 113pp; English.
XX
CC The present sequence is that of cDNA encoding human MAPKAP kinase 2.
CC MAPKAP kinase 2 is an example of a gene that is differentially expressed
CC in cancer cells relative to non-cancer cells, or between cancer cells of
CC different malignant potential. Such genes, and their gene products, can
CC be assayed in addition to tyrosine threonine kinase (TTK, see ABP54938),
CC in methods of the invention for differential expression in a test cell.

CC The invention is based on the finding that TTK is differentially
CC expressed in various forms of cancer. Methods are provided for the
CC identification of cancerous cells, especially breast cancer and colon
CC cancer cells, by detection of expression levels of TTK, as well as
CC diagnostic, prognostic and therapeutic methods based on differential
CC expression. These methods can be used as the basis of rational therapy.
CC Assays for identifying molecules that modulate the activity of these
CC genes in cancers, as well as methods of inhibiting tumour growth by
CC inhibiting the activity of TTK are also provided
XX
SQ Sequence 2263 BP; 496 A; 716 C; 618 G; 433 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.1e-134 Length: 2263
Score: 2006.50 Matches: 396
Percent Similarity: 68.9% Conservative: 0
Best Local Similarity: 68.9% Mismatches: 0
Query Match: 95.3% Indels: 179
DB: 6 Gaps: 1

US-10-469-221-2 (1-396) x ABV73995 (1-2263)

QY 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20
|||||
Db 391 TCCACGGCCAGAGCCCCCGGTGCGTTCCTCCCGCCCCCGCCGCGAGCCCCC 450

QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
|||||
Db 451 ACCCTGCCCTGCCGACACCCCCCGCGCAGCCCGCCGCGCGAGTTCCTCCG 510

QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspTyrLys 60
|||||
Db 511 CAGTTCCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGACTACAAG 570

QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
|||||
Db 571 GTCACCAGCCAGGTCTCTGGGGCTGGGCATCAACGGCAAAGTTTTTGACATCTTCAACAAG 630

QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
|||||
Db 631 AGGACCCAGGAGAAATTTCGCCCTCAAAATGCTTCAGGACTGCCCCAAGCCCGCAGGGAG 690

QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
|||||
Db 691 GTGGAGCTGCACTGGCGGGCTCCAGTGCCCGCACATCGTACGGATCGTGGATGTGTAC 750

QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
|||||
Db 751 GAGAACTCTGTAGCAGGAGGAAAGTGCCTGCTGATTGTCATGGAATGTTTGGACGGTGA 810

QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
|||||
Db 811 GAACTCTTTAGCCGAATCCAGGATCCAGGATCCAGGAGACCAGGCATTTCACAGAAAGAGAAGCATCC 870

QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
|||||
Db 871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 930

QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
|||||
Db 931 CGGGATGTCAAGCCTGAGAATCTCTATACACCTCCAAAAGGCCCAACGCCATCTCTGAAA 990

QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
|||||
Db 991 CTCACCTGACTTTGGCTTTGCCAAGGAAACCACCAGCCACAACCTCTTTGACCACCTCCTTGT 1050

QY 221 TyrThrProTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
|||||
Db 1051 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAAGTATGACAAAGTCTGT 1110

QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrPropheTyr 260
|||||
Db 1111 GACATGTGTCCTGGGTGTTCATCATGTACATCTCTGTGTGGGTATCCCCCCTTCTAC 1170

QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 1171 TCCAACCACGGCCTTGCCATCTCTCCGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 1231 GAATTTCCTCCCAACCCAGATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 1291 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGG 1350
QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1351 ATCATGCAATCAACAAAGTCCCTCAAAACCCACTGCACACAGCCGGGTCCTGAAGGAG 1410
QY 341 AspLysGluArgTrpGluAspValLys----- 349
Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGGTGTCTTCATGACAAGAACAGCAGCAGGCC 1470
QY 349 ----- 349
Db 1471 ACTTGGCTGACCAGGTTGTGAGCAGAGGATTCTGTGTTCCTGTCCAAACTCAGTGTGTT 1530
QY 349 ----- 349
Db 1531 TCTTAGAATCCTTTTATTCCTGGGTCTCTAATGGGACCTTAAAGACCATCTGGTATCAT 1590
QY 349 ----- 349
Db 1591 CTTCTCATTTTGCAGAAGAGAAACTGAGGCCACAGAGCGGAGGCAGTCTGTCTCAAGGTC 1650
QY 349 ----- 349
Db 1651 ACGCAGCTGGTGACTGGTTGGGCAGACCCGACCCAGGTTTCTGACTCCTGGCCCAAGT 1710
QY 349 ----- 349
Db 1711 CTCTTCTCCTATCCTCGGGATCACTGGGGGCTCTCAGGGAACAGCAGCAGTGCCATA 1770
QY 349 ----- 349
Db 1771 GCCAGGCTCTCTGTGCTGCCAGCGCTGGGGTGAGGCTGCCGTTGTGTCAGCGTGACCACTAA 1830
QY 349 ----- 349
Db 1831 CCAGCCCGTCTTCTCTCTGTCTGTCTCCACCCCTGCGGCCCTCACCCCTGCCCTTGTGTCTC 1890
QY 349 ----- 349
Db 1891 TGTCTCTCACGTCCTCTTCTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1950
QY 350 -----GluGluMetThrSerAlaLeuAlaThrMetArgVal 361
Db 1951 TTCCTGTGTGCTGCCGTGCCCCAGGAGGAGATGACCACTGCTTGGCCACAATGCGCGTT 2010
QY 362 AspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLys 381
Db 2011 GACTACGAGCAGATCAAGATAAAAGATTGAGATGCATCCAACCCCTCTGCTGTCTGAAG 2070
QY 382 ArgArgLysLysAlaArgAlaLeuGluAlaAlaAlaLeuAlaHis 396
Db 2071 AGCGGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCCAC 2115

RESULT 10

ACA62272

ID ACA62272 standard; DNA; 2263 BP.

XX ACA62272;

AC ACA62272;

DT 11-AUG-2003 (first entry)

XX

DE Human DNA encoding MAPKAP kinase 2.
XX Human; ds; gene; tyrosine threonine kinase; TTK; cancer; cytostatic;
KW mitotic checkpoint gene; MAPKAP kinase 2.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 379..1491
FT /*tag= a
FT /product= "MAPKAP kinase 2"
XX
PN US2003045491-A1.
XX
PD 06-MAR-2003.
XX
PF 21-FEB-2002; 2002US-00081119.
PR 23-FEB-2001; 2001US-0289813P.
XX
PA (REIN/) REINHARD C.
PA (JEFF/) JEFFERSON A B.
PA (CHAN/) CHAN V W.
XX Reinhard C, Jefferson AB, Chan VW;
PI
XX
DR WPI; 2003-456566/43.
DR P-PSDB; ABU61622.
XX

Detecting cancer in a subject, by comparing expression levels of tyrosine threonine kinase polypeptide or polynucleotide in a subject cell and a normal cell, where an increase in the expression level in the test cell is indicative of cancer.

Disclosure; Page 59-61; 79pp; English.

The invention relates to detecting cancer (other than ovarian cancer) in a subject, comprising comparing the expression levels of tyrosine threonine kinase (TTK, a mitotic checkpoint gene) polypeptide or polynucleotide in a test cell obtained from the subject and in a normal non-cancer cell, where an increase in the expression level of TTK protein or nucleic acid in the test cell compared to that in the normal cell, indicates the presence of cancer other than ovarian cancer. Also included are reducing growth of a cancerous cell (by contacting a cancerous cell with an amount of an agent effective to reduce TTK polypeptide activity in the cell), an assay for identifying a candidate agent that reduces growth of a cancerous cell (comprising: (i) detecting the activity of a TTK polypeptide in the presence of a candidate agent; and (ii) comparing the activity of TTK polypeptide in the presence of a candidate agent relative to TTK polypeptide activity in the absence of a candidate agent), identifying an agent that reduces TTK activity (comprising: (i) contacting a cancerous cell displaying elevated expression of a TTK-encoding polynucleotide with a candidate agent; and (ii) determining the effect of the candidate agent on TTK polypeptide activity) and assessing the prognosis of a cancerous disease other than ovarian cancer in a subject (comprising: (i) detecting expression of TTK -encoding polynucleotide in a test cancer cell of a subject; and (ii) comparing a level of expression of TTK-encoding polynucleotide in the test cancer cell with a level of expression of the polynucleotide in a control non-cancer cell, where the level of expression of TTK in the test cancer cell relative to the level of expression in the control non-cancer cell is indicative of the prognosis of the cancerous disease). The methods are useful for detecting cancer (other than ovarian cancer) in a subject, reducing growth of cancerous cells, identifying a candidate agent that reduces growth of a cancerous cell, identifying an agent that reduces TTK activity and assessing the prognosis of a cancerous disease other than ovarian cancer. The methods are also useful for determining the ability of a subject to respond to a particular therapy e.g. as a basis of rational therapy. The present sequence encodes another protein which is differentially expressed in cancer tissues, in this case human MAPKAP kinase 2

Sequence 2263 BP; 496 A; 716 C; 618 G; 433 T; 0 U; 0 Other;

Alignment Scores:		4.1e-134	Length:	2263
Pred. No.:		2006.50	Matches:	396
Score:		68.9%	Conservative:	0
Percent Similarity:		68.9%	Mismatches:	0
Best Local Similarity:		95.3%	Indels:	179
Query Match:		9	Gaps:	1
DB:				
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QY	1	SerGlnGlyGlnSerProValProPheProAlaProAlaProProProGlnProPro	20	
Db	391	TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCGCCCGCGCCCGCAGCCCCC	450	
QY	21	ThrProAlaLeuProHisProProAlaGlnProProProProProGlnGlnPhePro	40	
Db	451	ACCCCTGCCCTGCCGACCCCGCGCGAGCGCGCGCCCGCCCGCCCGCAGATTCCCG	510	
QY	41	GlnPheHisVallySerGlyLeuGlnIleLysLysAsnAlaIleIleAspAspTyrLys	60	
Db	511	CAGTTCACAGTCAAGTCCGGCTGCAGATCAAGAAGAACGCCATCATCGATACAAG	570	
QY	61	ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys	80	
Db	571	GTCACCAAGCCAGTCTGGGGCTGGGCATCAACGGCAAAAGTTTGGCAGATCTTCAACAAG	630	
QY	81	ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu	100	
Db	631	AGGACCCAGGAGAAATTGCCCCTCAAAATGCTTCAGGACTGCCCCCAAGGCCCGCAGGGAG	690	
QY	101	ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr	120	
Db	691	GTGGAGCTGCACCTGGCGGCCTCCACAGTGCCTGCTGATTGTATGGAATGTTGGACGGTGTAC	750	
QY	121	GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly	140	
Db	751	GAGAACTCTGTACGAGGGAGGAAGTGCCCTGCTGATTGTATGGAATGTTGGACGGTGA	810	
QY	141	GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer	160	
Db	811	GAACCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGAGCATCC	870	
QY	161	GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis	180	
Db	871	GAAATCATGAAGACCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT	930	
QY	181	ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys	200	
Db	931	CGGGATGTCAAGCCTGAGAAATCTTTATACACTCCAAAAGGCCCAACGCCATCCTTGAA	990	
QY	201	LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys	220	
Db	991	CTCACTGACTTTGGCTTTGCCAAGGAAACCACCAAGCCACAACTCTTTGACCACTCCTTGT	1050	
QY	221	TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys	240	
Db	1051	TATACACCGTACTATGTGGCTCCAGAAGTGCTGGTCCAGAGAAGTATGACAAGTCTCTGT	1110	
QY	241	AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr	260	
Db	1111	GACATGTGGTCCCTGGGTGTCATCATGTATACATCTCTGTGTGGGTATCCCCCTTCTAC	1170	
QY	261	SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr	280	
Db	1171	TCCAAACCACGGCCTTGCCATCTCTCCGGGCATGAGACTCGCATCCGAATGGGCCAGTAT	1230	
QY	281	GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn	300	
Db	1231	GAATTTCCCAACCCAGAAATGGTCAGAAATATCAGAGGAAGTGAAGATGCTATTCCGAAT	1290	
QY	301	LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp	320	

Db	1291	CTGCTGAAAAACAGAGCCCAACAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGG	1350	
QY	321	IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu	340	
Db	1351	ATCATGCAATCAACAAAGGTCCTCAAAACCCCACTGCACACCAAGCCGGTCTCTGAAGGAG	1410	
QY	341	AspLysGluArgTrpGluAspValLys-----	349	
Db	1411	GACAAGGAGCGGTGGGAGGATGTCAAGGGGTGTTCTTATGACAAGAACAGCAGCAGGCC	1470	
QY	349	-----	349	
Db	1471	ACTTGGCTGACCAGGTTGTGAGCAGAGGATTCTGTGTTCCCTGTCCAAACTCAGTGCTGTT	1530	
QY	349	-----	349	
Db	1531	TCTTAGAATCCTTTTATTCCCTGGGTCTCTAATGGGACCTTAAAGACCATCTGGTATCAT	1590	
QY	349	-----	349	
Db	1591	CTTCTCATTTTGCAGAAAGAAACTGAGGCCCAGAGCGGAGGGCAGTCTGCTCAAGGTC	1650	
QY	349	-----	349	
Db	1651	ACGAGCTGGTGACTGGTTGGGGCAGACCGGACCCAGGTTTCTGACTCCTGGCCCCAAGT	1710	
QY	349	-----	349	
Db	1711	CTCTTCCTCTATCTCTGCGGGATCACTGGGGGGCTCTCAGGGAAACAGCAGCAGTGCCATA	1770	
QY	349	-----	349	
Db	1771	GCCAGGCTCTCTGCTGCCCAGCGCTGGGGTGAGGCTGCCGCTTGTGACGCTGGACCACTAA	1830	
QY	349	-----	349	
Db	1831	CCAGCCCGTCTTCTCTCTCTCTCCACCCCTGCCGCCCTCACCCCTGCTTGTGTCTC	1890	
QY	349	-----	349	
Db	1891	TGCTCTCACGTCTCTCTTCTGTGTCTCTCTCTACCTGTCTTCTGGGCTCTCTGTACCC	1950	
QY	350	-----GluGluMetThrSerAlaLeuAlaThrMetArgVal	361	
Db	1951	TTCTCTGGTCTGCCGTGCCCCCAAGGAGAGATGACCAGTGCCTTGGCCACAATGCCGCTT	2010	
QY	362	AspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLys	381	
Db	2011	GACTACGAGCAGATCAAGATAAAAGATTGAAGATGCATCCAACCCCTCTGCTGCTGAAG	2070	
QY	382	ArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis	396	
Db	2071	AGGCGGAAGAAAGCTCGGGCCCTGGAGGCTCGGCTCTGGCCCCAC	2115	
RESULT 11				
ADM36337				
ID	ADM36337	standard; cDNA; 2263 BP.		
XX	XX			
AC	ADM36337;			
XX	XX			
DT	03-JUN-2004	(first entry)		
XX	XX			
DE	Human MK2	variant 1 encoding cDNA SEQ ID NO:1.		
XX	XX			
KW	KW	ischaemic injury;		
KW	KW	mitogen-activated protein kinase-activated protein kinase 2; MK2;		
KW	KW	vasotropic; cerebroprotective; cardiant; hypotensive;		
KW	KW	antiarteriosclerotic; thrombolytic; neuroprotective; cardiovascular;		
KW	KW	antianiginal; antiarrhythmic; MK2 antagonist; cerebral ischaemia;		
KW	KW	ischaemia; vascular occlusion; cerebral infarction; stroke;		
KW	KW	cerebral vascular disease; myocardial infarction;		
KW	KW	coronary artery disease; congestive heart failure;		
KW	KW	unstable angina; high blood pressure; claudication;		

KW peripheral occlusive arterial disease; atherosclerosis;
KW thrombotic condition; thromboembolic condition; CNS disorder; human;
XX MK2 variant 1; chromosome 1q32; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 379..1491

FT /*tag= a
FT /product= "MK2 variant 1"

XX WO2004017909-A2.

XX PD 04-MAR-2004.

XX PF 21-AUG-2003; 2003WO-US026337.

XX PR 23-AUG-2002; 2002US-0405586P.

XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX PI Wang X, Schieven G, Feuerstein GZ;

XX DR WPI; 2004-226726/21.

XX DR P-PSDB; ADM36338.

PT Reducing or treating ischemic injury, comprises administering an
PT inhibitor of mitogen-activated protein kinase-activated protein kinase 2
PT (MK2) activity or expression.

XX PS Disclosure; SEQ ID NO 1; 39pp; English.

XX
CC The present invention describes a method for reducing ischaemic injury in
CC a mammal, which comprises administering a compound that reduces the
CC activity of mitogen-activated protein kinase-activated protein kinase 2
CC (MK2) or that inhibits MK2 expression. Also described: (1) identifying a
CC compound which inhibits MK2 expression in a cell, or which modulates MK2
CC activity; (2) compounds identified by the method above; and (3) treating
CC ischaemic injury by administering to a patient a compound above, or an
CC MK2 modulator. The compound has vasotropic, cerebroprotective, cardiant,
CC hypotensive, antiarteriosclerotic, thrombolytic, neuroprotective,
CC cardiovascular, antianginal and antiarrhythmic activities, and can be
CC used as an MK2 antagonist. The method is useful reducing or treating
CC ischaemic injury, particularly cerebral ischaemia. Compounds identified
CC by the method are useful for treating ischaemia, (e.g. ischaemia
CC resulting from vascular occlusion, cerebral infarction, stroke, and
CC related cerebral vascular diseases), myocardial infarction, coronary
CC artery disease, congestive heart failure, cardiac arrhythmias, unstable
CC angina, high blood pressure, claudication, peripheral occlusive arterial
CC disease, atherosclerosis, thrombotic or thromboembolic conditions, or CNS
CC disorders associated with cerebral ischaemia. The present sequence
CC encodes the human MK2 variant 1, which is located on chromosome 1q32.

XX SQ Sequence 2263 BP; 496 A; 716 C; 618 G; 433 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.1e-134 Length: 2263
Score: 2006.50 Matches: 396
Percent Similarity: 68.9% Conservative: 0
Best Local Similarity: 68.9% Mismatches: 0
Query Match: 95.3% Indels: 179
DB: 12 Gaps: 1

US-10-469-221-2 (1-396) x ADM36337 (1-2263)

QY 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20
Db 391 TCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCGCGCCCGCGCGAGCCCCC 450

QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProProGlnPhePro 40

Db 451 ACCCCTGCCCTGCCGACCCCCCGCGCGAGCCCGCGCGCCCGCGCGAGTTCCCG 510

QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleLeuAspTyrLys 60
Db 511 CAGTTCACGTCAGTCCGGCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 570
QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 571 GTCACCAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAG 630
QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu 100
Db 631 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCAAGGCCGAGGAG 690
QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 691 GTGGAGCTGCACCTGGCGGGCCTCCCAGTCCCGCACATCGTACGGATCGTGATGTGTAC 750
QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 751 GAGAAATCTGTACGACAGGGAGGAAGTGCCTGCTGATGTGATGGAATGTTTGGACGGTGA 810
QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 811 GAAACTCTTTAGCCGAATCCAGGATCGAGGAGACCCAGGCATTACAGAAAGAGAGCATCC 870
QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAATCAATGCCCCAT 930
QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 931 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAGGCCCAACGCCATCCTGAAA 990
QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 991 CTCACGTGACTTTGGCTTTGCCAAGGAAACCCAGCCACAACCTCTTTGACCACTCCTTGT 1050
QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 1051 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGGTCCAGAGAAAGTATGACAAAGTCTCT 1110
QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 1111 GACATGTGTCCTCGGTGTTCATCATGTATCATCTGCTGTGTGGGTATCCCCCTTCTAC 1170
QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 1171 TCCAACCCAGCCCTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGCCAGTAT 1230
QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 1231 GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGTCATTCGGAAT 1290
QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 1291 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCC 1350
QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1351 ATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCCAGCCGGGTCTCTGAAGGAG 1410
QY 341 AspLysGluArgTrpGluAspValLys----- 349
Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGGTGTCTTCATGACAAGAACAGCGACCGAGGCC 1470
QY 349 ----- 349
Db 1471 ACTTGGCTGACCAGGTTGTGAGCAGAGGATTCTGTGTTCTCTGTCCAAACTCAGTGTGTT 1530
QY 349 ----- 349
Db 1531 TCTTAGAATCCTTTTATTCCCTGGGTCTCTAATGGGACCTTAAAGACCATCTGGTATCAT 1590
QY 349 ----- 349

Db 1591 CTTCTCATTTTGCAGAAGAGAAACTAGGCCCCAGAGGCGGAGGCAGTCTGTCTCAAGGTC 1650
QY 349 ----- 349
Db 1651 ACGCAGCTGGTGACTGGTTGGGCAGACCGGAGCCAGGTTTCCTGACTCTCTGGCCCAAGT 1710
QY 349 ----- 349
Db 1711 CTCTTCCTCCTATCTCTCGGGATCACTGGGGGGCTCTCAGGGAACAGCAGCAGTGCCATA 1770
QY 349 ----- 349
Db 1771 GCCAGGCTCTCTGTGCCAGCGCTGGGTGAGGCTGCCGTTGTACGCTGGACCACTAA 1830
QY 349 ----- 349
Db 1831 CCAGCCCGTCTTCTCTCTCTGTCTCCACCCCTGCCGCCCTCACCCCTGCGCTTGTGTCTC 1890
QY 349 ----- 349
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QY 350 -----GluGluMetThrSerAlaLeuAlaThrMetArgVal 361
Db 1951 TTCTTGGTGTGCGGTGCCCCCAGGAGGAGATGACCAGTGCCCTTGCCACAAATGCGCGTT 2010
QY 362 AspTyrGluGlnIleLysLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLys 381
Db 2011 GACTACGAGCAGATCAAGATAAAAAGATTGAAGATGCATCCAACCCCTCTGTGCTGAAG 2070
QY 382 ArgArgLysLysAlaArgAlaLeuGluAlaAlaAlaLeuAlaHis 396
Db 2071 AGCGGAAGAAAGCTCGGGCCCTGGAGGCTCGGGCTCTGGCCCCAC 2115
RESULT 12
ADX06657
ID ADX06657 standard; DNA; 2263 BP.
XX
AC ADX06657;
XX
DT 21-APR-2005 (first entry)
XX
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1222.
XX
KW cytotstatic; cyclin-dependent kinase; cdk; biomarker; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2005012875-A2.
XX
PD 10-FEB-2005.
XX
PF 29-JUL-2004; 2004WO-US024424.
XX
PR 29-JUL-2003; 2003US-0490890P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX
DR WPI; 2005-163068/17.
DR P-PSDB; ADX06658.
XX
PT Biomarkers useful for predicting or determining the response of a mammal
PT to a cancer treatment comprising administration of a modulator of cyclin-
PT dependent kinase activity.
XX
PS Claim 5; SEQ ID NO 1222; 141pp; English.
XX
CC This invention describes a novel method of predicting or determining
CC whether a mammal will respond or is responding to an anti-cancer agent
CC that modulates cyclin-dependent kinase (cdk) activity. The method

CC comprises measuring the level of one or more biomarkers selected from
CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
CC invention is utilized in a kit for determining or predicting whether
CC patient would be susceptible or resistant to treatment by an agent
CC modulating cdk activity. The invention also describes a method for
CC utilizing individualized genetic profiles for treating diseases and
CC disorders based on patient's response and molecular level, specialized
CC microarrays comprising the biomarkers described, antibodies directed
CC against the biomarkers and a cell culture model to identify biomarkers.
CC The cdk modulator is preferably N-5-([5-(1,1-Dimethylethyl)-2-
CC oxazolyl]methylthio]-2-thiazolyl)-4-piperidine carboxamide, 0.5-L-
CC tartaric acid salt. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct sequences. This
CC sequence encodes a biomarker used in the method of the invention.
XX
SQ Sequence 2263 BP; 496 A; 716 C; 618 G; 433 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.1e-134 Length: 2263
Score: 2006.50 Matches: 396
Percent Similarity: 68.9% Conservative: 0
Best Local Similarity: 68.9% Mismatches: 0
Query Match: 95.3% Indels: 179
DB: 14 Gaps: 1

US-10-469-221-2 (1-396) x ADX06657 (1-2263)
QY 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20
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QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProProGlnPhePro 40
Db 451 ACCCTGCTGCTGCGCACCCCCCGCGCAGCCGCCGCCGCCGCCGCCGCCGCCGCC 510
QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspTyrLys 60
Db 511 CAGTTCCACGTCAAGTCCGGCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 570
QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 571 GTCACCAGCCAGGTCTTGGGGCTGGGCATCAACGGCAAAGTTTTGCAGATCTTCAACAAG 630
QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Db 631 AGGACCCAGAGAGAAATTTCGCCCTCAAAATGCTTCAGGACTGCCCCCAAGGCCGAGGAG 690
QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 691 GTGGAGCTGCACCTGGCGGCCCTCCCGAGTGCCCTGCTGATTGTCATGGAATGTTGGACGGTGA 750
QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 751 GAGAATCTGTACGCAGGAGGAGGAGTGCCTGCTGATTGTCATGGAATGTTGGACGGTGA 810
QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 811 GAACTCTTTAGCCGAATCCAGGATCCAGGATCGAGGAGACCAGGCATTCACAGAAAGAGAAGCATCC 870
QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTTCAATCAACATTTGCCCAT 930
QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 931 CGGGATGTCAAGCCTGAGAAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 990
QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 991 CTCAC TGACTTTGGCTTTGCCAAGGAAACACACAGCCACAACTCTTTGACCACTCCTTGT 1050

QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 1051 TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCTGT 1110
QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 1111 GACATGTGGTCCCTGGGTGTATCATGTATCATCCTGTGTGGGTATCCCCCTTCTAC 1170
QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 1171 TCCAACACCGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 1231 GAATTCCCAACCCAGATGGTCAGAAATATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 1291 CTGCTGAAAACAGAGCCCCACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCTTGG 1350
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QY 341 AspLysGluArgTrpGluAspValLys----- 349
Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGGTGCTTTCATGACAAGAACAGCGACCAAGGCC 1470
QY 349 ----- 349
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QY 349 ----- 349
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QY 349 ----- 349
Db 1711 CTCTTCCTCCTATCCTGCGGATCACTGGGGGGCTCTCAGGGAACAGCAGCAGTGCCATA 1770
QY 349 ----- 349
Db 1771 GCCAGGCTCTCTGTGCCAGCGCTGGGGTGAGGCTGCCGTTGTGACGGTGGAACCACTAA 1830
QY 349 ----- 349
Db 1831 CCAGCCCGTCTTCTCTCTCTGTCTCCACCCCTGCCGCCCTCACCCCTGCCCTTGTGTCTC 1890
QY 349 ----- 349
Db 1891 TGTCTCTCACGTCTCTCTTCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1950
QY 350 -----GluGluMetThrSerAlaLeuAlaThrMetArgVal 361
Db 1951 TTCTTGGTGTGCGCGTCCCCCAGGAGGATGACCAAGTGCCTTGGCCACAATGGCGTT 2010
QY 362 AspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLys 381
Db 2011 GACTACGAGCAGATCAAGATAAAAGATTGAAGATGCATCCAACCCCTCTGTGTCTGAAG 2070
QY 382 ArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 2071 AGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCAC 2115

ADY86797
ID ADY86797 standard; DNA; 2263 BP.
XX
AC ADY86797;
XX
DT 02-JUN-2005 (first entry)
XX
DE Human MAPKAP kinase 2 gene, SEQ ID NO: 33.
XX
KW Prognosis; cancer; cytostatic; neoplasm;
KW mitogen-activated protein kinase-activated protein kinase 2; MAPKAPK2;
KW gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 379..1491
FT /*tag= a
FT /product= "Human MAPKAP kinase 2 protein"
XX
PN US2005063974-A1.
XX
PD 24-MAR-2005.
XX
PF 27-SEP-2004; 2004US-00951477.
XX
PR 21-FEB-2001; 2001US-0271254P.
PR 23-FEB-2001; 2001US-0289813P.
PR 21-FEB-2002; 2002US-00081119.
XX
PA (REIN/) REINHARD C.
PA (JEFF/) JEFFERSON A B.
PA (CHAN/) CHAN V W.
XX
PI Reinhard C, Jefferson AB, Chan VW;
XX
DR WPI; 2005-241248/25.
DR P-PSDB; ADY86798.
XX
PT Assessment of prognosis of a cancerous disease other than ovarian cancer
PT comprises detection and comparison of expression of a tyrosine threonine
PT kinase-encoding polynucleotide in a test cancer cell with a control non-
PT cancer cell.
XX
PS Disclosure; SEQ ID NO 33; 78pp; English.
XX
CC The invention relates to a method for assessing the prognosis of a
CC cancerous disease other than ovarian cancer which involves detection and
CC comparison of expression of a tyrosine threonine kinase (TTK)-encoding
CC polynucleotide in a test cancer cell with a control non-cancer cell. The
CC method is useful to assess the prognosis of a cancerous disease other
CC than ovarian cancer. It is useful to identify cancerous cells and to
CC determine the ability of a subject to respond to a particular therapy
CC e.g. as the basis of rational therapy. The present sequence is the human
CC mitogen-activated protein kinase-activated protein kinase 2 (MAPKAPK2)
CC gene. This sequence is differentially expressed in cancerous cells.
XX
SQ Sequence 2263 BP; 496 A; 716 C; 618 G; 433 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.1e-134 Length: 2263
Score: 2006.50 Matches: 396
Percent Similarity: 68.9% Conservative: 0
Best Local Similarity: 68.9% Mismatches: 0
Query Match: 95.3% Indels: 179
DB: 14 Gaps: 1

US-10-469-221-2 (1-396) x ADY86797 (1-2263)

QY 1 SerGlnGlyGlnSerProValProPheProAlaProAlaProGlnProPro 20
Db 391 TCCAGGGCCAGAGCCCGCGGTGCCGTTCCTCCCGCCCCCGCCGCGAGCCCCC 450

Db 1319 GACAAAGGAGCGGTGGGAGGATGTCAAGGGTGTCTTCATGACAAGAACAGCGACCAGGCC 1378
QY 349 ----- 349
Db 1379 ACTTGGCTGACCAGGTTGTGACGAGAGGATTCTGTGTTCTGTCCAAACTCAGTGTCTGTT 1438
QY 349 ----- 349
Db 1439 TCTTAGAATCCTTTTATTCCCTGGGTCTCTAATGGGACCTTAAAGACCATCTGGTATCAT 1498
QY 349 ----- 349
Db 1499 CTTCTCATTTTGCAGAAAGAAAACTGAGGCCCCAGAGGCGGAGGGCAGTCTGCTCAAAGGTC 1558
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Db 1559 ACGCAGCTGGTGA CTGTTGGGGCAGACCGGACCCAGGTTTCCTGACTCCTGGCCCAAGT 1618
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QY 349 ----- 349
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QY 349 ----- 349
Db 1739 CCAGCCCGTCTTCTCTCTGTCTGCCACCCCTGCCGCCCTCACCCCTGCCCTTGTGTCTC 1798
QY 349 ----- 349
Db 1799 TGTCTCTCACGTCTCTCTCTGTGTCTCTCTACCTGTCTTCTGGCTCTCTCTGTACCC 1858
QY 350 -----GluGluMetThrSerAlaLeuAlaThrMetArgVal 361
Db 1859 TTCTTGGTGTGCCGTGCCCCCAGGAGGAGATGACCACTGTCCTTGCCCACTATGCCGTT 1918
QY 362 AspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeuLys 381
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QY 382 ArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 19, 2006, 15:44:17 ; Search time 1565 Seconds
(without alignments)
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Minimum DB seq length: 0
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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2	2106	100.0	1203	8	US-10-469-221-3	Sequence 3, Appli
3	2097	99.6	1726	8	US-10-645-190-3	Sequence 3, Appli
4	2078	98.7	1336	8	US-10-641-643-1397	Sequence 1397, Ap
5	2006.5	95.3	2263	6	US-10-081-119-33	Sequence 33, Appl
6	2006.5	95.3	2263	8	US-10-645-190-1	Sequence 1, Appli
7	2006.5	95.3	2263	10	US-10-951-389-33	Sequence 33, Appl
8	2006.5	95.3	2263	10	US-10-951-406-33	Sequence 33, Appl
9	2006.5	95.3	2263	10	US-10-951-477-33	Sequence 33, Appl
10	2006.5	95.3	2263	10	US-10-977-087-33	Sequence 33, Appl
11	2006.5	95.3	3608	10	US-10-887-553A-633	Sequence 633, App
12	1991.5	94.6	2258	3	US-09-964-824A-261	Sequence 261, App
13	1991.5	94.6	2258	7	US-10-305-720-1415	Sequence 1415, Ap
14	1991.5	94.6	2258	10	US-10-843-641A-5564	Sequence 5564, Ap
15	1925.5	91.4	2802	3	US-09-925-300-238	Sequence 238, App
16	1729	82.1	1305	7	US-10-338-411-30	Sequence 30, Appl
17	1729	82.1	1305	8	US-10-389-640-30	Sequence 30, Appl
18	1716	81.5	981	8	US-10-294-027-5	Sequence 5, Appli
19	1709	81.1	1168	16	US-11-128-061-3380	Sequence 3380, Ap
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22	1391	66.0	2481	8	US-10-298-354-4	Sequence 4, Appli
23	1391	66.0	2481	11	US-10-501-035-160	Sequence 160, App
24	1391	66.0	2481	16	US-11-122-329-65	Sequence 65, Appl
25	1201	57.0	2000	13	US-11-097-143-5663	Sequence 5663, Ap
26	1201	57.0	2025	13	US-11-097-143-29036	Sequence 29036, A
27	1043	49.5	6276	13	US-11-097-143-5662	Sequence 5662, Ap
28	1043	49.5	6276	13	US-11-097-143-29035	Sequence 29035, A
29	847	40.2	480	9	US-10-723-860-658	Sequence 658, App
30	847	40.2	480	10	US-10-756-149-685	Sequence 685, App
31	784.5	37.3	2060	10	US-10-770-726-24	Sequence 24, Appl
32	784.5	37.3	2060	16	US-11-152-366-5	Sequence 5, Appli
33	784.5	37.3	2066	16	US-11-152-366-6	Sequence 6, Appli
34	783.5	37.2	1968	8	US-10-717-597-326	Sequence 326, App
35	783.5	37.2	1968	10	US-10-872-645-2	Sequence 2, Appli
36	717	34.0	600	16	US-11-128-061-7022	Sequence 7022, Ap
37	717	34.0	600	16	US-11-128-049-7022	Sequence 7022, Ap
38	712	33.8	496	3	US-09-918-995-4551	Sequence 4551, Ap
39	698.5	33.2	758	3	US-09-910-943-446	Sequence 446, App
40	666.5	31.6	1669	10	US-10-491-467-55	Sequence 55, Appl
41	622	29.5	477	7	US-10-062-674-280	Sequence 280, App
42	586.5	27.8	483	3	US-09-918-995-23785	Sequence 23785, A
43	540	25.6	3061	3	US-09-880-107-2146	Sequence 2146, Ap
44	540	25.6	3206	7	US-10-159-563-155	Sequence 155, App
45	540	25.6	3206	10	US-10-517-328-48	Sequence 48, Appl

ALIGNMENTS

RESULT 1
US-10-469-221-1
; Sequence 1, Application US/10469221
; Publication No. US20040170995A1
; GENERAL INFORMATION:
; APPLICANT: LOGRASSO, PHILIP
; APPLICANT: HAWKINS, JULIO
; APPLICANT: LISNOCK, JEAN MARIE
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: A NOVEL HUMAN SIGNAL TRANSDUCING KINASE-MAPKAP-2; ENCODED
; TITLE OF INVENTION: PROTEINS, CELLS TRANSFORMED THEREWITH AND USES THEREOF
; FILE REFERENCE: 20813P
; CURRENT APPLICATION NUMBER: US/10/469,221
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: PCT/US02/05670
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/272,260
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Human
US-10-469-221-1

Alignment Scores:									
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Score:	2106.00	Matches:	396						
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Query Match:	100.0%	Indels:	0						
DB:	8	Gaps:	0						
US-10-469-221-2 (1-396) x US-10-469-221-1 (1-1191)									
QY	1	SerGlnGlyGlnSerProValProPheProAlaProAlaProProGlnProPro	20						
Db	1	TCCCAGGGCCAGAGCCCGCGGTGCCGTCCCCCGCCCGCCCGCGCAGCCCCC	60						
QY	21	ThrProAlaLeuProHisProProAlaGlnProProProProProGlnGlnPhePro	40						
Db	61	ACCCCTGCCCTGCCGACCCCCCGGCGCAGCCGCGCCCGCCCGCAGATTCCCG	120						
QY	41	GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleAspAspTyrLys	60						
Db	121	CAGTTCACGTCGAAGTCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG	180						
QY	61	ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys	80						
Db	181	GTCACCAGCCAGGTCCTGGGCTGGGCATCAACGGCAAGTTTTGCAGATCTTCAACAAG	240						
QY	81	ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu	100						
Db	241	AGGACCCAGGAGAAATTCCGCCCTCAAAATGCTTCAGGACTGCCCCAAGGCCCGCAGGGAG	300						
QY	101	ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr	120						
Db	301	GTGGAGCTGCACTGGCGGGCCTCCCACTGCCCGCACATCGTACGGATCGTGGATGTGTAC	360						
QY	121	GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly	140						
Db	361	GAGAAATCTGTACGAGGGAGGAAGTGCCTGCTGATGTGTATGTAAGTGTGGACGGTGA	420						
QY	141	GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer	160						
Db	421	GAACCTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGAGCATCC	480						
QY	161	GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis	180						
Db	481	GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT	540						
QY	181	ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys	200						
Db	541	CGGGATGTCAAGCCTGAGAAATCTTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA	600						
QY	201	LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys	220						
Db	601	CTCACTGACTTTGGCTTTGCCAAGGAAACCACGAGCCACAACCTCTTTGACCACTCCTTGT	660						
QY	221	TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys	240						
Db	661	TATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAGTATGACAAGTCCCTGT	720						
QY	241	AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr	260						
Db	721	GACATGTGGTCCCTGGGTGTCATCATGTACATCCTGCTGTGTGGGTATCCCCCTTCTAC	780						
QY	261	SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr	280						
Db	781	TCCAAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT	840						
QY	281	GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn	300						
Db	841	GAATTTCCCAACCCAGAAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT	900						
QY	301	LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp	320						

QY	321	IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu	340						
Db	961	ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACACGCGGGTCTCTGAAGGAG	1020						
QY	341	AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg	360						
Db	1021	GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAGTGCCTTGGCCACAATGCGC	1080						
QY	361	ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeu	380						
Db	1081	GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACCTCTGTGCTGTG	1140						
QY	381	LysArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis	396						
Db	1141	AAGAGCGGAAGAAAGCTCGGCGCCTGGAGGCTGCGGCTCTGGCCAC	1188						
RESULT 2									
US-10-469-221-3									
; Sequence 3, Application US/10469221									
; Publication No. US20040170995A1									
; GENERAL INFORMATION:									
; APPLICANT: LOGRASSO, PHILIP									
; APPLICANT: HAWKINS, JULIO									
; APPLICANT: LISNOCK, JEAN MARIE									
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING									
; TITLE OF INVENTION: A NOVEL HUMAN SIGNAL TRANSDUCING KINASE-MAPKAP-2; ENCODED									
; TITLE OF INVENTION: PROTEINS, CELLS TRANSFORMED THEREWITH AND USES THEREOF									
; FILE REFERENCE: 20813P									
; CURRENT APPLICATION NUMBER: US/10/469,221									
; CURRENT FILING DATE: 2003-08-27									
; PRIOR APPLICATION NUMBER: PCT/US02/05670									
; PRIOR FILING DATE: 2002-02-25									
; PRIOR APPLICATION NUMBER: 60/272,260									
; PRIOR FILING DATE: 2001-02-28									
; NUMBER OF SEQ ID NOS: 4									
; SOFTWARE: FastSEQ for Windows Version 4.0									
; SEQ ID NO 3									
; LENGTH: 1203									
; TYPE: DNA									
; ORGANISM: Human									
US-10-469-221-3									
Alignment Scores:									
Pred. No.:	1.28e-211	Length:	1203						
Score:	2106.00	Matches:	396						
Percent Similarity:	100.0%	Conservative:	0						
Best Local Similarity:	100.0%	Mismatches:	0						
Query Match:	100.0%	Indels:	0						
DB:	8	Gaps:	0						
US-10-469-221-2 (1-396) x US-10-469-221-3 (1-1203)									
QY	1	SerGlnGlyGlnSerProValProPheProAlaProAlaProProGlnProPro	20						
Db	13	TCCCAGGGCCAGAGCCCGCGGTGCGGTCCCGCCCGCGCCCGCGCAGCCCCC	72						
QY	21	ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro	40						
Db	73	ACCCCTGCCCTGCCGACCCCGCGCGCAGCCCGCGCGCGCGCGCAGTTCGCG	132						
QY	41	GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleAspAspTyrLys	60						
Db	133	CAGTTCACGTCGAAGTCGGCCTGCAGATCAAGAAGAACGTCATCATGACTACAAG	192						
QY	61	ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys	80						
Db	193	GTACACAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAG	252						
QY	81	ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu	100						
Db	253	AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG	312						


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QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 313 GTGGAGCTGCACTGGCGGCTCCAGTGCCTCCGCACATCGTACGGATCGTGGTGTGTAC 372
QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 373 GAGAACTCTGTACGCAGGGAGGAAGTGCCTGTGATTGTATGGAATGTTTGGACGGTGA 432
QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 433 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTACAGAAAGAGAAGCATCC 492
QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 493 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 552
QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 553 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAA 612
QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 613 CTCACGTACTTTGGCTTTGCCAAGGAAACCACCGCACAACTCTTTGACCACTCCTTGT 672
QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 673 TATACACCGTACTATGTGGCTCCAGAAGTGTGGGTCCAGAGAAGTATGACAAGTCCTGT 732
QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 733 GACATGTGTCCTCGGTGTGCATCATGTATCATCTGCTGTGTGGTATCCCGCTTCTAC 792
QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 793 TCCAACCACGGCTTGCCATCTCTCCGGGCATGAAGACTGCATCCGAATGGGCCAGTAT 852
QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 853 GAATTTCCCAACCCAGAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTATTGGGAAT 912
QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 913 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 972
QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 973 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCAGCCGGTCTCTGAAGGAG 1032
QY 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360
Db 1033 GACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCAGTGCCCTTGGCCACAATGCCG 1092
QY 361 ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeu 380
Db 1093 GTTGACTACGAGCAGATCAAGATAAAAAGATTGAAGATGCATCCAACCTCTGCTGCTG 1152
QY 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 1153 AAGAGCGGAAGAAGCTCGGGCCCTGGAGGCTGGGGCTCTGGGCCAC 1200
RESULT 3
US-10-645-190-3
; Sequence 3, Application US/10645190
; Publication No. US20040110710A1
; GENERAL INFORMATION:
; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
; TITLE OF INVENTION: METHODS FOR PREVENTING ISCHEMIC BRAIN INJURY
; FILE REFERENCE: D0299 NP
; CURRENT APPLICATION NUMBER: US/10/645,190
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/405,586
; PRIOR FILING DATE: 2002-08-23
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; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1726
; TYPE: DNA
; ORGANISM: Human
US-10-645-190-3
Alignment Scores:
Pred. No.: 1.9e-210 Length: 1726
Score: 2097.00 Matches: 395
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.6% Indels: 0
DB: 8 Gaps: 0
US-10-469-221-2 (1-396) x US-10-645-190-3 (1-1726)
QY 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20
Db 391 TCCAGGGCCAGAGCCCGCGGTGCCGTTCCTCCCGCCCGCCCGCCCGCCAGCCCCC 450
QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProProGlnPhePro 40
Db 451 ACCCTTGCCCTGCCGCACCCCGCGCGCAGCGCGCCCGCCCGCCCGCCAGTCCCG 510
QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspAspTyrLys 60
Db 511 CAGTTCCACGTCAGTCCGGCTGCAGATCAAGAAGAACGTCATCATCGACTACAAG 570
QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 571 GTCACCAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAG 630
QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Db 631 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCAAGCCCGCAGGGAG 690
QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 691 GTGGAGCTGCATGGCGGGCTCCCGAGTGCCTCCCGACATCGTACGGATCGTGGATGTGTAC 750
QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 751 GAGAACTCTGTACGCAGGAGGAAGTGCCTGTGATTGTATGGAATGTTTGGACGGTGA 810
QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 811 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTACAGAAAGAGAAGCATCC 870
QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 930
QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 931 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCCATCTCTGAAA 990
QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 991 CTCACGTACTTTGGCTTTGCCAAGGAAACCAACAGCCACAACTCTTTGACCACCTCCTTGT 1050
QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 1051 TATACACCGTACTATGTGGCTCCAGAAGTGTGGTCCAGAGAAGTATGACAAGTCCCTGT 1110
QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 1111 GACATGTGTCCTGGGTGTTCATCATGTACATTCTGCTGTGTGGTATCCCCCTTCTAC 1170
QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 1171 TCCAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
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Qy 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 1231 GAATTTCACCAACCAGAAATGGTCAGAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 1291 CTGCTGAAACACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 1350
Qy 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1351 ATCATGCAATCAACAAGGTCCTCAAAACCCCACTGCACACCAAGCGGGTCCTGAAGGAG 1410
Qy 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360
Db 1411 GACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTGGCCACAATGCGC 1470
Qy 361 ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeu 380
Db 1471 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACCCCTCTGCTGCTG 1530
Qy 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 1531 AAGAGCGGAAGAAGCTCGGGCCCTGGAGGCTCGGCTCTGGCCCAAC 1578

RESULT 4

US-10-641-643-1397
; Sequence 1397, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1397:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g407074
; SEQUENCE DESCRIPTION: SEQ ID NO: 1397 :
US-10-641-643-1397

Alignment Scores:
Pred. No.: 1.34e-208 Length: 1336
Score: 2078.00 Matches: 393
Percent Similarity: 99.2% Conservative: 0
Best Local Similarity: 99.2% Mismatches: 3
Query Match: 98.7% Indels: 0
DB: 8 Gaps: 0
US-10-469-221-2 (1-396) x US-10-641-643-1397 (1-1336)
Qy 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20
Db 1 TCCCAGGGCCAGAGCCCGCGTGCCTTCCCGCCCCCGCGCGCGAGCCCCC 60
Qy 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
Db 61 ACCCTGCCCTGCCGCAACCCCGGGCAGCCGCGCGCGCGCGAGTTCCTCG 120
Qy 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspTyrLys 60
Db 121 CAGTTCACAGTCAAGTCCGGCTCGCAGATCAAGAGAACGCCATCATCGATGACTACAAG 180
Qy 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 181 GTCACCAGCCAGGTCTCGGGCTGGGCATCAACGGCAAAGTTTTCAGAGATCTTCAACAAG 240
Qy 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Db 241 AGGACCCAGGAGAAATTCCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCGCGAGGAG 300
Qy 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 301 GTGGAGCTGACTGGCGGGCTCCAGTGCCCCGACATCGTACGGATCGTGGATGTGTAC 360
Qy 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 361 GAGAACTGTACGCAGGAGGAGGAGTGCCTGCTGATTGTTCATGGAATGTTTGGACGGTGA 420
Qy 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 421 GAACTCTTAGCCGAATCCAGGATCCAGGATCCAGGAGACCAGGCATTACAGAGAAAGAGACATCC 480
Qy 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 540
Qy 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 541 CGGGATGTCAAGCCTGAGAATCTCTATACACCTCCAAAAGGCCCAACGCCCATCTCTGAAA 600
Qy 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 601 CTCACCTGACTTTGGCTTTGCCAAGGAAACCAACAGCCACAACCTTTGACCACCTCCTTGT 660
Qy 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 661 TATACACCGTACTATGTGGCTCCAGAAGTGTGGTCCAGAGAGATATGACAAGTCTCTGT 720
Qy 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProPheTyr 260
Db 721 GACATGTTGGTCTCGGTGTCAATGATACATTCTGCTGTGTGGGTATCCCCCTTCTAC 780
Qy 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 781 TCCAACCACGGCCTTGCCATCTCTCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
Qy 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 841 GAAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
Qy 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320

Db 901 CTGCTGAAACAGAGCCCAACCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGG 960

QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340

Db 961 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACACGACCGGGTCTCTGAAGGAG 1020

QY 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360

Db 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTGGCCACAATGCGC 1080

QY 361 ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeu 380

Db 1081 GTTGACTACGAGCAGATCAAGATAAAAGATTGAAGATGCATCCAACCCCTCTGCTGCTG 1140

QY 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396

Db 1141 AAGAGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCAAC 1188

RESULT 5

US-10-081-119-33

; Sequence 33, Application US/10081119

; Publication No. US20030045491A1

; GENERAL INFORMATION:

; APPLICANT: Reinhard, Christoph

; APPLICANT: Jefferson, Anne B.

; APPLICANT: Chan, Vivien W.

; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic

; TITLE OF INVENTION: Target in Cancer

; FILE REFERENCE: 16932.002

; CURRENT APPLICATION NUMBER: US/10/081,119

; CURRENT FILING DATE: 2002-02-21

; PRIOR APPLICATION NUMBER: 60/289,813

; PRIOR FILING DATE: 2001-02-21

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 33

; LENGTH: 2263

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (379) ... (1491)

US-10-081-119-33

Alignment Scores:

Pred. No.: 1e-200 Length: 2263

Score: 2006.50 Matches: 396

Percent Similarity: 68.9% Conservative: 0

Best Local Similarity: 68.9% Mismatches: 0

Query Match: 95.3% Indels: 179

DB: 6 Gaps: 1

US-10-469-221-2 (1-396) x US-10-081-119-33 (1-2263)

QY 1 SerGlnGlyGlnSerProProValPropheProAlaProAlaProProGlnProPro 20

Db 391 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCGCCGCCCGGCCCGGCCCGCCAGCCCCC 450

QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnPhePro 40

Db 451 ACCCTGTCCTGCCGACCCCGCGCAGCCCGCGCCCGCCCGCCCGCCAGATTCCCG 510

QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleAspAspTyrLys 60

Db 511 CAGTTCACCGTCAAGTCCGGCCTGCAGATCAAGAGAACGCCATCATCGATGACTACAAG 570

QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80

Db 571 GTCACCAAGCCAGGTCTCTGGGGCTGGGCATCAACGCAAAAGTTTTCAGATCTTCAACAAG 630

QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu 100

Db 631 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 690

QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120

Db 691 GTGGAGCTGCACTGGCGGGCCTCCCAGTCCCGCACATCGTACGGATCGTGGATGTGTAC 750

QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140

Db 751 GAGAATCTGTACCGAGGAGGAAGTGCCTGTGATTGTATGGAATGTTTGGACGGTGA 810

QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160

Db 811 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTACAGAAAGAGAAGCATCC 870

QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180

Db 871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 930

QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200

Db 931 CGGGATGTCAAGCCTGAGAATCTCTTATACACTCCAAAGGCCCAACGCCATCCTGAAA 990

QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220

Db 991 CTCACCTGACTTTGGCTTTGCCAAGGAACACACGACCACAACTCTTTGACCACTCCTGT 1050

QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240

Db 1051 TATACACCGTACTATGTGGTCCAGAAAGTGTGGGTCCAGAGAAAGTATGACAAAGTCCTGT 1110

QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260

Db 1111 GACATGTGGTCCCTGGGTGTTCATCATGTATCATCTGCTGTGGTATCCCCCTTCTAC 1170

QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280

Db 1171 TCCAACCAACGCGCTTGCCATCTCTCCGGSCATGAAGACTCGCATCCGAATGGCCAGTAT 1230

QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300

Db 1231 GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290

QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320

Db 1291 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 1350

QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340

Db 1351 ATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCAGCCGGGTCTCTGAAGGAG 1410

QY 341 AspLysGluArgTrpGluAspValLys----- 349

Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGGTGTCTTCATGACAAGAACAGCGACGAGGCC 1470

QY 349 ----- 349

Db 1471 ACTTGGCTGACCAGGTTGTGAGCAGAGGATTCTGTGTTCCCTGTCCAAACTCAGTGTGTT 1530

QY 349 ----- 349

Db 1531 TCTTAGAATCCTTTTATTCCCTGGGTCTCTAATGGGACCTTAAAGACCATCTGGTATCAT 1590

QY 349 ----- 349

Db 1591 CTTCTCATTTTGCAGAAAGAGAAACTGAGGCCCCAGAGCGGAGGGGAGTCTGCTCAAGGTC 1650

QY 349 ----- 349

Db 1651 ACGCAGCTGGTGACTGGTTGGGGCAGACCGGACCCAGGTTTCTTGACTCTTGCCCAAGT 1710

QY 349 ----- 349

Db 1711 CTCTTCCTCTATCTCTCGGGATCACTGGGGGGCTCTCAGGGGAACAGCAGCAGTGCCATA 1770


```
Qy      349 ----- 349
Db      1771 GCAGGCTCTCTGTCGCCAGCGTGGGTGAGGCTGCCGTTGTGAGCGTGGACCACTAA 1830
Qy      349 ----- 349
Db      1831 CCAGCCCGTCTTCTCTCTCTGTCCTCCACCCCTGCCGCCCTCACCCCTGCCCTTGTGTCTC 1890
Qy      349 ----- 349
Db      1891 TGTCCTCAGCTCTCTCTCTGCTGTCTCTCCTACCTGTCTTCTGGCTCTCTCTGTACCC 1950
Qy      350 -----GluGluMetThrSerAlaLeuAlaThrMetArgVal 361
Db      1951 TTCTTGGTGTGCCGTGCCGCCAGGAGAGATGACCAGTGCCTTGGCCACAATGCGCGTT 2010
Qy      362 AspTyrGluGlnIleLysIleLysIleGluAspAlaSerAsnProLeuLeuLys 381
Db      2011 GACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACCCCTCTGCTGCTGAAG 2070
Qy      382 ArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db      2071 AGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCAC 2115

RESULT 7
US-10-951-389-33
; Sequence 33, Application US/10951389
; Publication No. US20050058627A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,389
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (379) ... (1491)
US-10-951-389-33

Alignment Scores:
Pred. No.:      1e-200      Length:      2263
Score:          2006.50      Matches:      396
Percent Similarity: 68.9%      Conservative: 0
Best Local Similarity: 68.9%      Mismatches: 0
Query Match:      95.3%      Indels:      179
DB:              10          Gaps:        1

US-10-469-221-2 (1-396) x US-10-951-389-33 (1-2263)

Qy      1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20
Db      391 TCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCC 450
Qy      21 ThrProAlaLeuProHisProProAlaGlnProProProProProProGlnGlnPhePro 40
Db      451 ACCCTGCCCTGCCGCAACCCCGCGGCGAGCCCGCGCGCGCGCGCGCGCGCGCGCGCG 510
Qy      41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspAspTyrLys 60
Db      511 CAGTTCCACGTCAGTCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 570
```

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Qy      61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db      571 GTCACCAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAAGTTTTGCAGATCTTCAACAAG 630
Qy      81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Db      631 AGGACCCAGGAGAAATTGCCCCCTCAAAATGCTTCAGGACTGCCCCAAGGCCCGCAGGGAG 690
Qy      101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db      691 GTGGAGCTGCACCTGGCGGGCCTCCCAGTGCCCGGCACATCGTACGGATCGTGGATGTGTAC 750
Qy      121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db      751 GAGAATCTGTACGCAAGGAGGAAGTGCCCTGCTGATTGTCTATGGAATGTTTGGACGGTGA 810
Qy      141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db      811 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTCACAGAAAGAGAAGCATCC 870
Qy      161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db      871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 930
Qy      181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db      931 CGGGATGTCAAGCTGAGAAATCTCTTATACACTCCAAAAGGCCCAACGCCATCTCTGAAA 990
Qy      201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db      991 CTCACCTGACTTTGGCTTTGCCAAGGAAACCAACCAGCCACAACTCTTTGACCACTCCTTGT 1050
Qy      221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db      1051 TATACACCGTACTATGTGGCTCCAGAAGTGTGGGTCCAGAGAAGTATGACAAGTCTCTGT 1110
Qy      241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProPropheTyr 260
Db      1111 GACATGTGGTCCCTGGGTGTCATCATGTATACATCCTGCTGTGTGGGTATCCCCCTTCTAC 1170
Qy      261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db      1171 TCCAACCAACGGCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGATGGGCCAGTAT 1230
Qy      281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db      1231 GAATTTCCCAACCCAGAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
Qy      301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db      1291 CTGCTGAAAAACAGAGCCCAACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCCCTTG 1350
Qy      321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db      1351 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCAGCCGGGTCTCTGAAGGAG 1410
Qy      341 AspLysGluArgTrpGluAspValLys----- 349
Db      1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGGTGTCTTCATGACAAGAACAGCAGCAGGCC 1470
Qy      349 ----- 349
Db      1471 ACTTGGCTGACCAGGTTGTGAGCAGAGGATTCTGTGTTCTCTCCAAACTCAGTGCTGTT 1530
Qy      349 ----- 349
Db      1531 TCTTAGAATCCTTTATTCCCTGGGTCTCTAATGGGACCTTAAAGACCATCTGGTATCAT 1590
Qy      349 ----- 349
Db      1591 CTTCTCATTTTGCAGAAGAGAAACTGAGGCCCCAGAGCGGAGGGCAGTCTGCTCAAGGTC 1650
```

```
QY      349  ----- 349
Db      1651  ACGCAGCTGGTGAAGTGGGGCAGACCGGACCCAGGTTTCCTGACTCCTGGCCCAAGT 1710
QY      349  ----- 349
Db      1711  CTCCTCCTATCCTGCGGGATCACTGGGGGCTCTCAGGGAACAGCAGCAGTGCCATA 1770
QY      349  ----- 349
Db      1771  GCCAGGCTCTGCTGCCAGCGCTGGGGTGAGGCTGCCGTTGTACGCTGGACCACTAA 1830
QY      349  ----- 349
Db      1831  CCAGCCCGTCTCTCTCTCTGCTGCCACCCCTGCCGCCCTCACCCCTGCCCTTGTGTCTC 1890
QY      349  ----- 349
Db      1891  TGTCTCTCACGCTCTCTCTGCTGTCTCTCTCTACCTGTCTCTCTGGCTCTCTGTACCC 1950
QY      350  -----GluGluMetThrSerAlaLeuAlaThrMetArgVal 361
Db      1951  TTCCTGGTGTGCGTGCCTCCAGGAGGAGATGACCAAGTGCCTTGGCCACAATGCGGTT 2010
QY      362  AspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLys 381
Db      2011  GACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACCTCTCTGCTGAAG 2070
QY      382  ArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db      2071  AGCGGAAGAAAGCTCGGGCCCTGGAGGCTCGGGCTCTGGCCAC 2115
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RESULT 8

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US-10-951-406-33
; Sequence 33, Application US/10951406
; Publication No. US20050059630A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,406
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (379) ... (1491)
US-10-951-406-33
```

Alignment Scores:

```
Pred. No.:      1e-200      Length:      2263
Score:          2006.50      Matches:      396
Percent Similarity: 68.9%      Conservative: 0
Best Local Similarity: 68.9%      Mismatches: 0
Query Match:      95.3%      Indels:      179
DB:              10          Gaps:        1
```

US-10-469-221-2 (1-396) x US-10-951-406-33 (1-2263)

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QY      * 1 SerGlnGlyGlnSerProValProPheProAlaProAlaProProGlnProPro 20
Db      391  TCCTCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCGGCCCCCGCGCGAGCCCCC 450
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```
QY      21  ThrProAlaLeuProHisProProAlaGlnProProProProProGlnGlnPhePro 40
Db      451  ACCCCTGCCCTGCCGACCCCGCGCGCAGCCCGCGCGCGCGCGCGCGCGCGCGCGCG 510
QY      41  GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleAspAspTyrLys 60
Db      511  CAGTTCACAGTCAAGTCCGGCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 570
QY      61  ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db      571  GTCACCAAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG 630
QY      81  ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Db      631  AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCAAGGCCCGCAGGAG 690
QY      101  ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db      691  GTGGAGCTGCACCTGGCGGGCTCCAGTGCCTGCATCGTACGGATCGTGGATGTGTAC 750
QY      121  GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db      751  GAGAACTCTGTACGACGAGGAGGAAAGTGCCTGCTGATTGTATGTAATGTTTGGACGGTGA 810
QY      141  GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db      811  GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCAATCACAGAAAAGAGAAGCATCC 870
QY      161  GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db      871  GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCAATCAATCAACATTTGCCCAT 930
QY      181  ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db      931  CGGGATGTCAAGCCTGAGAATCTTTATACACCTCCAAAAGSGCCCAACGCCATCCTGAAA 990
QY      201  LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db      991  CTCACCTGACTTTGGCTTTGCCAAGGAAACCACCGCCCAACTCTTTGACCACCTCCTTGT 1050
QY      221  TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db      1051  TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAAGTCTGT 1110
QY      241  AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProPheTyr 260
Db      1111  GACATGTGTCCTGGGTGTCATCATGTATCATCTCTGTGTGGGTATCCCCCTTCTAC 1170
QY      261  SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db      1171  TCCAACCAAGCGCTTGCCATCTCTCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
QY      281  GluPheProAsnProGluTyrSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db      1231  GAATTTCCCAACCCAGAAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
QY      301  LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTyr 320
Db      1291  CTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 1350
QY      321  IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db      1351  ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCGCGGGTCTCTGAAGGAG 1410
QY      341  AspLysGluArgTrpGluAspValLys----- 349
Db      1411  GACAAGGAGCGGTGGGAGGATGTCAAGGGGTGTCTTTCATGACAAGAACAGCGACCGGCC 1470
QY      349  ----- 349
Db      1471  ACTTGGCTGACCAGGTTGTGAGCAGAGGATTTCTGTGTTCTGTCTCCAAACTCAGTGTGTT 1530
```



```
QY 349 ----- 349
Db 1531 TCTTAGAATCCTTTTATTCCCTGGGTCTCTAATGGGACCTTAAAGACCAATCTGGTATCAT 1590
QY 349 ----- 349
Db 1591 CTTCTCATTTTGCAGAAAGAAAACTGAGGCCAGAGCGGAGGGCAGTCTGCTCAAGGTC 1650
QY 349 ----- 349
Db 1651 ACGCAGCTGGTACTGGTTGGGGCAGACCGGACCCAGGTTTCTGACTCCTTGSCCAAGT 1710
QY 349 ----- 349
Db 1711 CTCTTCCTCCTATCCTGCGGATCACTGGGGGGCTCTCAGGGAACAGCAGCAGTGCCATA 1770
QY 349 ----- 349
Db 1771 GCCAGGCTCTCTGCTGCCCAGCGCTGGGGTGAGGCTGCCGTTGTGACGGTGACCACTAA 1830
QY 349 ----- 349
Db 1831 CCAGCCCGTCTTCTCTCTGTGCTCCACCCCTGCCGCCCTCACCCCTGCCCTTGTGTCTC 1890
QY 349 ----- 349
Db 1891 TGTCTCTACGTCTCTCTTCTGTCTGTCTCTCCTACCTGTCTTCTGGCTCTCTGTACCC 1950
QY 350 -----GluGluMetThrSerAlaLeuAlaThrMetArgVal 361
Db 1951 TTCTTGGTGTGCCGTGCCCGCCAGGAGGATGACCAAGTGCCTTGGCCACAATGCGCGTT 2010
QY 362 AspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLys 381
Db 2011 GACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACCCCTCTGCTGAAG 2070
QY 382 ArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 2071 AGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCAC 2115
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RESULT 9

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US-10-951-477-33
; Sequence 33, Application US/10951477
; Publication No. US20050063974A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,477
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (379) ... (1491)
US-10-951-477-33

Alignment Scores:
Pred. No.: 1e-200 Length: 2263
Score: 2006.50 Matches: 396
Percent Similarity: 68.9% Conservative: 0
Best Local Similarity: 68.9% Mismatches: 0
```

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Query Match: 95.3% Indels: 179
DB: 10 Gaps: 1
US-10-469-221-2 (1-396) x US-10-951-477-33 (1-2263)
QY 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20
Db 391 TCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCCGGCCCCCGCAGCCCCC 450
QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProProGlnPhePro 40
Db 451 ACCCTGCCCTGCCGACCCCCCGCGCAGCGCGCGCGCCCCCGCAGCAGTCCCG 510
QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleAspTyrLys 60
Db 511 CAGTTCCACGTCAAGTCCGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAG 570
QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 571 GTCACCAGCCAGTCTGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAG 630
QY 81 ArgThrGlnGlyLysPheAlaLeuLysMetIleuGlnAspCysProLysAlaArgGlu 100
Db 631 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCCAAGGCCGAGGAG 690
QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 691 GTGGAGCTGCACTGGCGGGCTCCAGTCCCGCACATCGTACGGATCGTGGATGTGTAC 750
QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 751 GAGAATCTGTACGACGAGGAGGAAGTGCCTGCTGATGTGATGGAATGTTGGACGGTGA 810
QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 811 GAACTCTTTAGCCGAATCCAGGATCGAGGAGAGACCAGGCATTCACAGAAAGAGAAGCATCC 870
QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAACATTTGCCAT 930
QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 931 CGGGATGTCAAGCCTGAGAATCTCTTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 990
QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 991 CTCACCTGACTTTGGCTTTGCCAAGGAAACACCAGCCACAACTCTTTGACCACTCCTTGT 1050
QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 1051 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGGTCCAGAGAAGTATGACAAAGTCTCTGT 1110
QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProPheTyr 260
Db 1111 GACATGTGTCCTGGGTGTCATCATGTATCATCTGCTGTGTGGGTATCCCCCTTCTAC 1170
QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 1171 TCCAAACCCAGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGCCAGTAT 1230
QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 1231 GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 1291 CTGCTGAAAAACAGAGCCCAACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCTTGG 1350
QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1351 ATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCAGCCGGGTCTCTGAAGGAG 1410
```


Db 931 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAGGCCCAACGCCATCCTGAAA 990
QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 991 CTCACGTGACTTTGGCTTTGGCAAGGAAACCAACCAAGCACAACTCTTTGACCACTCCTTGT 1050
QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 1051 TATACACCGTACTATGTGGTCTCCAGAAGTCTGGGTCCAGAGAAGTATGACAAGTCTCTGT 1110
QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 1111 GACATGTGGTCCCTGGGTGTCATCATGTACATCCTGCTGTGGGTATCCCCCTTCTAC 1170
QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 1171 TCCAAACCACGGCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
QY 281 GluPheProAsnProGluTrpSerGluValSerGluValLysMetLeuIleArgAsn 300
Db 1231 GAATTTCCCAACCCAGAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 1291 CTGCTGAAACACAGAGCCACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCTTGG 1350
QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1351 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCAGCCGGTCTTGAAGGAG 1410
QY 341 AspLysGluArgTrpGluAspValLys----- 349
Db 1411 GACAAGGAGCGGTGGAGGATGTCAAGGGGTGCTTCATGACAAGAACAGCGACCAAGGCC 1470
QY 349 ----- 349
Db 1471 ACTTGGCTGACCAAGGTGTGAGCAGAGGATTCGTGTTCCTGTCCAAACTCAGTGTGTT 1530
QY 349 ----- 349
Db 1531 TCTTAGAATCCTTTTAFTCCTTGGGTCTCTAATGGGACCTTAAGACCATCTGGTATCAT 1590
QY 349 ----- 349
Db 1591 CTTTCTCATTTTGCAGAAAGAAACTGAGGCCCCAGAGCGGAGGGCAGTCTGCTCAAGGTC 1650
QY 349 ----- 349
Db 1651 ACGCAGCTGGTGACTGGTTGGGCAGACCGGACCCAGGTTTCCTGACTCCTGGCCCCAAGT 1710
QY 349 ----- 349
Db 1711 CTCTTCTCCTATCTCGCGGGATCACTGGGGGGTCTCAGGGAACAGCAGCAGTGCCATA 1770
QY 349 ----- 349
Db 1771 GCCAGGCTCTCTGTGCCCCAGCGCTGGGGTGAGGCTGCCCTCACCCCTGCCCTTGTGTCTC 1830
QY 349 ----- 349
Db 1831 CCAGCCCGTCTTCTCTCTCTGTCTCCACCCCTGCGGCCCTCACCCCTGCCCTTGTGTCTC 1890
QY 349 ----- 349
Db 1891 TGTCTCTCACGTCTCTTCTGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1950
QY 350 -----GluGluMetThrSerAlaLeuAlaThrMetArgVal 361
Db 1951 TTCCTGGTGTGCGGTGCCCCCAGGAGGAGATGACCAGTGCCTTGGCCACAATGCGCGTT 2010
QY 362 AspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeuLys 381
Db 2011 GACTACGAGCAGATCAAGATAAAAAAAGATTGAAGATGCATCCAACCCCTCTGCTGCTGAAG 2070

QY 382 ArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 2071 AGCGGAAGAAAGCTCGGGCCCTGGAGGCTGGGCTCTGGCCCCAC 2115

RESULT 11

US-10-887-553A-633
; Sequence 633, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; with insulin signalling dysregulation
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; PRIOR FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 633
; LENGTH: 3608
; TYPE: DNA
; ORGANISM: human
US-10-887-553A-633

Alignment Scores:
Pred. No.: 1.93e-200 Length: 3608
Score: 2006.50 Matches: 396
Percent Similarity: 68.9% Conservative: 0
Best Local Similarity: 68.9% Mismatches: 0
Query Match: 95.3% Indels: 179
DB: 10 Gaps: 1

US-10-469-221-2 (1-396) x US-10-887-553A-633 (1-3608)

QY 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20
Db 299 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCTCCGCCCCCGCCGCGCAGCCCCC 358
QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProProGlnPhePro 40
Db 359 ACCCTGCTCCGCGCACCCCCCGGCGCAGCCGCGCCGCGCCGCGCAGTTCCTCG 418
QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleAspTyrLys 60
Db 419 CAGTTCCACGTCAAGTCCGGCTCGGCCTGCAGATCAAGAAGAACCCATCATCGATACAAG 478
QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 479 GTCACCAGCCAGGTCTTGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAG 538
QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgGlu 100
Db 539 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCAAGCCCGCAGGGAG 598
QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 599 GTGGAGCTGCACCTGGCGGGCTCCCGAGTCCCGCACATCGTACGGATCGTGGATGTGTAC 658
QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 659 GAGAACTCTGTACGCAGGAGGAAGTGCCTGTGATTGTTCATGGAATGTTTGGACGGTGA 718
QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 719 GAACTCTTTAGCCGAATCCAGGATCCAGGATCGAGGAGACCAGGCATTCACAGAAAGAGAAGCATCC 778
QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 779 GAAATCATGAAGAGCATCGGTGAGGCCCATCCAGTATCTGCAATTCATCAACATTTGCCCAT 838

QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 930
QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 931 CGGGATGTCAAGCCTGAGAAATCTTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 990
QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 991 CTCACCTGACTTTGGCTTTGCCAAGGAAACCAACGACACAACTCTTTTGACCACTCCTTGT 1050
QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 1051 TATACACCGTACTATGTGGTCCAGAGTGCTGGGTCCAGAGAAGTATGACAAATCCTGT 1110
QY 241 AspMetTyrSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 1111 GACATGTGGTCCCTGGGTGTCATCATGTACATCCTGTGTGGGTATCCCCCCTTCTAC 1170
QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 1171 TCCAAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
QY 281 GluPheProAsnProGluTyrSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 1231 GAATTTCCCAACCCAGAAATGGTCAGAAATATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTyr 320
Db 1291 CTGCTGAAAACAGAGCCACCCAGAGAATGACCATCACCGAGTTTATGAACACCCCTTGG 1350
QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1351 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCGCGGTCTCTGAAGGAG 1410
QY 341 AspLysGluArgTyrGluAspValLys----- 349
Db 1411 GACAAGGAGCGGTGGAGGATGTCAAGGGGTCTTCTATGACAAGAACAGCAGCAGGCC 1470
QY 349 ----- 349
Db 1471 ACTTGGCTGACCAGGTGTGAGCAGAGGATTCTGTGTTCTGTCCAAACTCAGTGTGTT 1530
QY 349 ----- 349
Db 1531 TCTTAGAATCCTTTTATTCCTTGGTCTCTAATGGGACCTTAAAGACCATCTGGTATCAT 1590
QY 349 ----- 349
Db 1591 CTCTCTATTTTGCAAGAGAGAAACTGAGGCCCAGAGCGGAGGCGAGTCTGCTCAAGGTC 1650
QY 349 ----- 349
Db 1651 ACGCAGCTGGTGACTGGTTGGGGCAGACCCGGACCCAGGTTTCTTGACTCCTGGCCCCAAGT 1710
QY 349 ----- 349
Db 1711 CTCTTCCCTATCCTGCGGGATCACTGGGGGGCTCTCAGGGAAACAGCAGCAGTGCCATA 1770
QY 349 ----- 349
Db 1771 GCCAGGCTCTCTGCTGCCACGCGCTGGGGTGAGGCTGCCGTGTGTACGCGTGGAACCACTAA 1830
QY 349 ----- 349
Db 1831 CCAGCCCGTCTTCTCTCTGTCTCCCAACCCCTGCCGCCCTCACCTGCCCTTGTGTCTCTG 1890
QY 349 ----- 349
Db 1891 TCTCTCACTGTCTCTTCTGTCT 1950

QY 350 -----GluGluMetThrSerAlaLeuAlaThrMetArgValAspTyr 363
Db 1951 GGTGTGCCGTGCCCCAGGAGGAGATGACCACTGCCTTGGCCACAATGCGCTTGACTA 2010
QY 363 rGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLysArgAr 383
Db 2011 CGAGCAGATCAACATAAAAAAGATTGAAGATGCATCCAACCCCTCTGCTGCTGAAGAGCG 2070
QY 383 gLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 2071 GAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCAC 2110
RESULT 13
US-10-305-720-1415
; Sequence 1415, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1415
; LENGTH: 2258
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g530089
US-10-305-720-1415
Alignment Scores:
Pred. No.: 3.83e-199 Length: 2258
Score: 1991.50 Matches: 396
Percent Similarity: 69.0% Conservative: 0
Best Local Similarity: 69.0% Mismatches: 0
Query Match: 94.6% Indels: 178
DB: 7 Gaps: 1
US-10-469-221-2 (1-396) x US-10-305-720-1415 (1-2258)
QY 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20
Db 391 TCCCAGGGCCAGAGCCCGCGGTGCGTTCCTCCCGCCCCCGCCGCGCAGCCCCC 450
QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
Db 451 ACCCTTGCCTGCCGACCCCGCGGCGAGCCCGCGCGCCCGCCGCGCAGTTCCTCCG 510
QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspTyrLys 60
Db 511 CAGTTCCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 570
QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 571 GTCACCAAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAAGTTTTCAGATCTTCAACAAG 630
QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Db 631 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCCAAGCCCGCAGGGAG 690
QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 691 GTGGAGCTGCACTGGCGGGCCTCCAGTCCCGCACATCGTACGATCGTGGATGTGTAC 750
QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 751 GAGAATCTGTACGAGGAGGAAGTGCCTGTGATTGTATGGAATGTTTGGACGGTGA 810

QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 811 GAACTCTTTAGCCGAATCCAGGATCGAGAGACCAGGCATTCACAGAAAGAGAGCATCC 870
QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 930
QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 931 CGGGATGTCAGCCTGAGAAATCTCTTATACACCTCCAAAAGSCCACAACGCATCCTGAAA 990
QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 991 CTCACTGACTTTGGCTTTGCCAAGGAACCAACCAGCCACAACCTCTTTGACCACTCCTTGT 1050
QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 1051 TATACACCGTACTATGTGGCTCCAGAAAGTGCTGGGTCCAGAGAAATGACAAAGTCCTGT 1110
QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 1111 GACATGTGTCCTGGGTGTCAATCATGTACATCCTGTGTGTGGGTATCCCCCTTCTAC 1170
QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 1171 TCCAAACCACGGCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 1231 GAATTTCCCAACCCAGAAATGGTCAGAAATATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 1291 CTGCTGAAAACAGAGCCCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 1350
QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1351 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCGCGGTCTCTGAAGGAG 1410
QY 341 AspLysGluArgTrpGluAspValLys----- 349
Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGTGTCATTATGACAAGAACAGCGACCAAGGCC 1470
QY 349 ----- 349
Db 1471 ACTTGGCTGACCAGGTGTGAGCAGAGGATTTGTGTTCCTGTCTCCAAACTCAGTGTGTT 1530
QY 349 ----- 349
Db 1531 TCTTAGAATCCTTTTATTCCTGGGTCTCTAATGGGACCTTAAAGACCATCTGGTATCAT 1590
QY 349 ----- 349
Db 1591 CTTCTCATTTTGCAAGAGAAACTGAGGCCCCAGAGCGGAGGCGAGTGTGCTCAAGGTC 1650
QY 349 ----- 349
Db 1651 ACGAGCTGGTGACTGGTTGGGCAGACCGGACCCAGGTTTCCTGACTCCTGGCCCCAAGT 1710
QY 349 ----- 349
Db 1711 CTCTTCTCCTATCCTGCGGGATCACTGGGGGCTCTCAGGGAACAGCAGCAGTGCCATA 1770
QY 349 ----- 349
Db 1771 GCCAGGCTCTCTGCTGCCCAGCGCTGGGTGAGGCTGCCGTTGTGACGCTGGAACCACTAA 1830
QY 349 ----- 349
Db 1831 CCAGCCCGTCTTCTCTCTGTCTCCACCCCTGCGGCCTCACCTGCCCTTGTGTCTGTG 1890
QY 349 ----- 349

Db 1891 TCCTCACTGTCTCTTCTGCTGTCTCTCTACTGTCTTCTGGCTCTCTCTGTACCCCTTCCT 1950
QY 350 -----GluGluMetThrSerAlaLeuAlaThrMetArgValAspTy 363
Db 1951 GGTGCTGCCGTGCCCCCAGGAGGAGATGACCAGTGCCTTGGCCACAATGCCGTTGACTA 2010
QY 363 rGluGlnIleLysIleLysIleGluAspAlaSerAsnProLeuLeuLysArgAr 383
Db 2011 CGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACCTCTGTGCTGAAGAGGCG 2070
QY 383 gLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 2071 GAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCCAC 2110

RESULT 14

US-10-843-641A-5564
; Sequence 5564, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5564
; LENGTH: 2258
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-5564

Alignment Scores:
Pred. No.: 3.83e-199 Length: 2258
Score: 1991.50 Matches: 396
Percent Similarity: 69.0% Conservative: 0
Best local Similarity: 69.0% Mismatches: 0
Query Match: 94.6% Indels: 178
DB: 10 Gaps: 1

US-10-469-221-2 (1-396) x US-10-843-641A-5564 (1-2258)

QY 1 SerGlnGlyGlnSerProProValProPheProAlaProAlaProProGlnProPro 20
Db 391 TCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCGCCCGCCCGCCCGCCCGCC 450
QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProProGlnGlnPhePro 40
Db 451 ACCCTGCTGCCGCACCCCCCGCGCAGCCCGCCCGCCCGCCCGCCCGCCAGTTC 510

QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspAspTyrLys 60
Db 511 CAGTTCACGTCAGTCGGCCTGCAGATCAAGAAAGCCCATCATCGACTACAAG 570
QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 571 GTCACAGCCAGGTCCTGGGCTGGGCATCAACGGAAAAGTTTGCAGATCTTCAACAAG 630
QY 81 ArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Db 631 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGACTGCCCAAGGCCCGCAGGGAG 690
QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 691 GTGGAGCTGCACCTGGCGGCCCTCCAGTGCCTCCGCACATCGTACGGATCGTGGATGTGTAC 750
QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 751 GAGAAATCTGTACGCGAGGAGGAAGTGCCTGCTGATGTGCATGGAATGTTTGGACGGTGA 810
QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 811 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCGAGCATTCACAGAAAGAGAGCATCC 870
QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATGCCCAT 930
QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
Db 931 CGGGATGTCAAGCCTGAGAATCTTTATACACCTCCAAAGGCCCAACGCCATCCTGAAA 990
QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 991 CTCACTGACTTTGGCTTTGCCAAGGAAACCAACGACCAAACTCTTTGACCACTCCTTGT 1050
QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 1051 TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAACTCCTGT 1110
QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 1111 GACATGTGTCCCTGGGTGTTCATCATGTATCATCTCTGTGTGGTATCCCCCTTCTAC 1170
QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 1171 TCCAACCAACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGCCAGTAT 1230
QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 1231 GAATTTCCCAACCCAGAAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 1291 CTGCTGAAAACAGAGCCCAACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCTTGG 1350
QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1351 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCAAGCCGCGGTCTGAAAGGAG 1410
QY 341 AspLysGluArgTrpGluAspValLys----- 349
Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGGTGTCTTCATGACAAGAACAGCAGCAGGCC 1470
QY 349 ----- 349
Db 1471 ACTTGGCTGACCAGGTTGTGAGCAGAGGATTCTGTGTTCTGTCCAAACTCAGTGCTGT 1530
QY 349 ----- 349
Db 1531 TCTTAGAATCCTTTTATTCCTGGGTCTCTAATGGGACCTTAAAGACCATCTGGTATCAT 1590
QY 349 ----- 349

Db 1591 CTTCTCATTTTCAGAAAGAAAACTGAGGCCCCAGAGGGCGAGTCTGCTCAAGGTC 1650
QY 349 ----- 349
Db 1651 ACGCAGCTGGTGACTGGTTGGGGCAGACCGGACCCAGGTTTCTCTGACTCTCTGGCCCCAAGT 1710
QY 349 ----- 349
Db 1711 CTCTTCCTCCATCCTGCGGGATCACTGGGGGGCTCTCAGGGAACAGCAGCAGTGCCATA 1770
QY 349 ----- 349
Db 1771 GCCAGGCTCTCTGCTGCCAGCGCTGGGTGAGGCTGCCGTTGTGACGCTGGACCACTAA 1830
QY 349 ----- 349
Db 1831 CCAGCCCGTCTTCTCTCTGCTGCCACCCCTGCCGCTCACCTGCCCTTGTGTCTCTG 1890
QY 349 ----- 349
Db 1891 TCTCTCACTGTCTTCTGCTGTCTCTCTACTGTCTTCTGGCTCTCTCTGTACCTTCT 1950
QY 350 -----GluGluMetThrSerAlaLeuAlaThrMetArgValAspTy 363
Db 1951 GGTGCTGCCGTGCCCCCAGGAGGAGATGACCATGTCCTTGGCCACAATGCGCGTTGACTA 2010
QY 363 rGluGlnIleLysLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLysArgAr 383
Db 2011 CGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACCCCTCTGCTGTAAGAGGCG 2070
QY 383 gLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 2071 GAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCAC 2110

RESULT 15
US-09-925-300-238
; Sequence 238, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 238
; LENGTH: 2802
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (613)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1800)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-238

Alignment Scores:
Pred. No.: 4.84e-192 Length: 2802
Score: 1925.50 Matches: 376
Percent Similarity: 94.7% Conservative: 0
Best Local Similarity: 94.7% Mismatches: 3
Query Match: 91.4% Indels: 19
DB: 3 Gaps: 1

US-10-469-221-2 (1-396) x US-09-925-300-238 (1-2802)

QY

1

SerGlnGlyGlnSerProValProPheProAlaProAlaProProGlnProPro

20

Db

40

TCCCAGGGCCAGAGCCCGCGGTGCTTCCCGCCCGCCG

81

QY

21

ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro

40

Db

82

-----CCGCGCCCGCCCGCAGAGTTCCCG

108

QY

41

GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleAaspAspTyrLys

60

Db

109

CAGTTCCACGTCAAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG

168

QY

61

ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys

80

Db

169

GTCACCAGCCAGGTCTTGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAG

228

QY

81

ArgThrGlnGlnLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu

100

Db

229

AGGACCCAGGAGAAATTCGCCCTCAAATGCTTCAGGACTGCCCCAGGCCCGCAG-GAG

287

QY

101

ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr

120

Db

288

GTGGAGCTGCACTGGCGGGCCTCCAGTGCCTGCTGATTGTTCATGGAAATGTTTGGACGGTGGTA

347

QY

121

GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly

140

Db

348

GAGAAATCTGTACGCGAGGGAGGAAGTGCTGCTGATTGTTCATGGAAATGTTTGGACGGTGGTA

407

QY

141

GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer

160

Db

408

GAACTCTTTAGCCGAATCCAGGATCGAGGACCAAGCATTCACAGAAAGAGAGCATCC

467

QY

161

GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis

180

Db

468

GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTTGCCCAT

527

QY

181

ArgAspValLysProGluAsnLeuTyrThrSerLysArgProAsnAlaIleLeuLys

200

Db

528

CGGGATGTCAGCCTGAGAAATCTCTTATACACCTCCAAAGGCCCAACGCCATCCTGAAA

587

QY

201

LeuThrAspPheGlyPheAlaLys-GluThrThrSerHisAsnSerLeuThrThrProCy

220

Db

588

CTCACTGACTTTGGCTTTGCCAAGGNAAACCAACGAGCCACAACCTCTTTGACCACTCCTTG

647

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240

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648

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707

QY

240

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260

Db

708

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767

QY

260

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280

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768

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827

QY

280

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300

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828

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887

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300

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320

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888

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947

QY

320

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340

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948

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1007

QY

340

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360

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1008

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1067

QY

360

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380

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1127

QY

380

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396

Db

1128

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1176

Search completed: June 19, 2006, 16:19:02
Job time : 1593 secs

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 19, 2006, 15:47:29 ; Search time 42 Seconds
(without alignments)
3329.070 Million cell updates/sec

Title: US-10-469-221-2
Perfect score: 2106
Sequence: 1 SQGQSPVPFPAPAPPQPP.....PLLLKRRKKARALEAALAH 396

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 290227 seqs, 117694381 residues

Total number of hits satisfying chosen parameters: 580454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:
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8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2106	100.0	3071	7	US-11-273-567-2 Sequence 2, Appli
2	2006.5	95.3	3608	7	US-11-273-567-1 Sequence 1, Appli
3	1391	66.0	2509	6	US-10-505-928-626 Sequence 626, App
4	799	37.9	574	6	US-10-488-619-2938 Sequence 2938, Ap
5	522	24.8	1740	7	US-11-242-505A-40 Sequence 40, Appl
6	522	24.8	1740	7	US-11-242-505A-41 Sequence 41, Appl
7	508.5	24.1	1937	6	US-10-449-902-20013 Sequence 20013, A
8	497	23.6	2641	6	US-10-449-902-21986 Sequence 21986, A
9	481	22.8	2524	6	US-10-449-902-26866 Sequence 26866, A

10	479	22.7	3982	6	US-10-505-928-350	Sequence 350, App
11	466	22.1	4098	7	US-11-293-697-891	Sequence 891, App
12	456	21.7	2392	6	US-10-449-902-18001	Sequence 18001, A
13	452	21.5	2163	6	US-10-449-902-7754	Sequence 7754, Ap
14	451.5	21.4	2365	6	US-10-449-902-17898	Sequence 17898, A
15	449.5	21.3	1764	6	US-10-953-349-903	Sequence 903, App
16	448	21.3	2127	6	US-10-449-902-26500	Sequence 26500, A
17	435.5	20.7	3552	7	US-11-312-958-33	Sequence 33, Appl
18	434.5	20.6	2390	6	US-10-449-902-22824	Sequence 22824, A
19	434	20.6	5703	7	US-11-312-958-63	Sequence 63, Appl
20	433	20.6	2313	6	US-10-449-902-18961	Sequence 18961, A
21	429.5	20.4	2252	6	US-10-449-902-16109	Sequence 16109, A
22	428	20.3	1545	7	US-11-217-529-372	Sequence 372, App
23	427.5	20.3	2044	6	US-10-449-902-23950	Sequence 23950, A
24	424.5	20.2	2254	6	US-10-449-902-4590	Sequence 4590, Ap
25	422	20.0	1311	7	US-11-217-529-79460	Sequence 79460, A
26	421	20.0	2514	7	US-11-217-529-2574	Sequence 2574, Ap
27	419	19.9	4726	7	US-11-312-958-3	Sequence 3, Appli
28	418	19.8	2421	7	US-11-312-958-35	Sequence 35, Appl
29	417	19.8	1341	7	US-11-217-529-76461	Sequence 76461, A
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31	412	19.6	2092	6	US-10-449-902-18743	Sequence 18743, A
32	411	19.5	1344	7	US-11-217-529-78535	Sequence 78535, A
33	410	19.5	2218	6	US-10-449-902-15987	Sequence 15987, A
34	408	19.4	1365	7	US-11-217-529-3295	Sequence 3295, Ap
c 35	403.5	19.2	1719	6	US-10-449-902-12406	Sequence 12406, A
36	400.5	19.0	1329	7	US-11-217-529-2931	Sequence 2931, Ap
37	399	18.9	2173	6	US-10-449-902-25032	Sequence 25032, A
38	397.5	18.9	1656	6	US-10-449-902-3549	Sequence 3549, Ap
39	397	18.9	1522	6	US-10-953-349-35112	Sequence 35112, A
40	394	18.7	1833	7	US-11-217-529-77728	Sequence 77728, A
41	393.5	18.7	1674	6	US-10-449-902-18507	Sequence 18507, A
42	391.5	18.6	2078	6	US-10-449-902-14918	Sequence 14918, A
43	386.5	18.4	2023	6	US-10-449-902-16670	Sequence 16670, A
44	386	18.3	2213	6	US-10-449-902-25149	Sequence 25149, A
45	384.5	18.3	1830	7	US-11-217-529-1793	Sequence 1793, Ap

ALIGNMENTS

RESULT 1
US-11-273-567-2
; Sequence 2, Application US/11273567
; Publication No. US20060115453A1
; GENERAL INFORMATION:
; APPLICANT: Yaffe, Michael B.
; APPLICANT: Manke, Isaac A.
; APPLICANT: Reinhardt, Hans Christian
; APPLICANT: Lim, Daniel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING CELLULAR PROLIFERATIVE DISEASES
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 01997/557002
; CURRENT APPLICATION NUMBER: US/11/273,567
; CURRENT FILING DATE: 2005-11-14
; PRIOR APPLICATION NUMBER: 60/627,352
; PRIOR FILING DATE: 2004-11-12
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 3071
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-273-567-2

Alignment Scores:
Pred. No.: 1.24e-144 Length: 3071
Score: 2106.00 Matches: 396
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-469-221-2 (1-396) x US-11-273-567-2 (1-3071)

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QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
Db 359 ACCCTGCCCTGCCGACCCCCCGCGAGCGCGCGCCCGCCCGCGCAGCAGTTCCCG 418
QY 41 GlnPheHisValLysSerGlyLeuGlnLysAsnAlaIleAspAspTyrLys 60
Db 419 CAGTTCCACGTCAGTCCGGCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 478
QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 479 GTCACCAAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTTTGCGATCTTCAACAAG 538
QY 81 ArgThrGlnGlnLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Db 539 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 598
QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 599 GTGGAGCTGCACCTGGCGGCCCTCCAGTGCCTGCACATCGTACGGATCGTGGATGTGTAC 658
QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 659 GAGAAATCTGTACGAGGGAGGAAGTGCCTGTGATTGTATGGAATGTTTGGACGGTGA 718
QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 719 GAACCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGAGCATCC 778
QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 779 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 838
QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
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QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
Db 899 CTCACGTACTTGGCTTTGCCAAGGAACCCACGAGCCACAACTCTTTGACCACACTCCTTGT 958
QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
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QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
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Db 1079 TCCAAACCACGGCCTTGCCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1138
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QY 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360
Db 1319 GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAGTGCCCTTGGCCACAATGCCG 1378

QY 361 ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeu 380
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QY 381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaAlaLeuAlaHis 396
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RESULT 2
US-11-273-567-1
; Sequence 1, Application US/11273567
; Publication No. US20060115453A1
; GENERAL INFORMATION:
; APPLICANT: Yaffe, Michael B.
; APPLICANT: Manke, Isaac A.
; APPLICANT: Reinhardt, Hans Christian
; APPLICANT: Lim, Daniel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING CELLULAR PROLIFERATIVE
; DISEASES
; FILE REFERENCE: 01997/557002
; CURRENT APPLICATION NUMBER: US/11/273,567
; CURRENT FILING DATE: 2005-11-14
; PRIOR APPLICATION NUMBER: 60/627,352
; PRIOR FILING DATE: 2004-11-12
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 3608
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-273-567-1
Alignment Scores:
Pred. No.: 2.55e-137 Length: 3608
Score: 2006.50 Matches: 396
Percent Similarity: 68.9% Conservative: 0
Best Local Similarity: 68.9% Mismatches: 0
Query Match: 95.3% Indels: 179
DB: 7 Gaps: 1
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Db 299 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCTCCCGCCCGCGCGCCAGCCCCC 358
QY 21 ThrProAlaLeuProHisProProAlaGlnProProProProGlnGlnPhePro 40
Db 359 ACCCTGCCCTGCCGACCCCCCGCGAGCGCGCGCCCGCGCAGCAGTTCCCG 418
QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleAspAspTyrLys 60
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QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
Db 479 GTCACCAAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTTTGCGATCTTCAACAAG 538
QY 81 ArgThrGlnGlnLysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGlu 100
Db 539 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 598
QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 599 GTGGAGCTGCACCTGGCGGCCCTCCAGTGCCTGCACATCGTACGGATCGTGGATGTGTAC 658
QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 659 GAGAAATCTGTACGAGGGAGGAAGTGCCTGTGATTGTATGGAATGTTTGGACGGTGA 718
QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 719 GAACCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGAGCATCC 778

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Qy	181	ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaileLeuLys	200
Db	611	CGAGATGTCAGCCCTGAAACCTACTCTACACATCTAAGGAGAAAGACGCAGTGCTTAAG	670
Qy	201	LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys	220
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Qy	221	TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys	240
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Qy	241	AspMetTrpSerLeuGlyValileMetTyrIleLeuLeuCysGlyTyrProProPheTyr	260
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Qy	261	SerAsnHisGlyLeuAlaileSerProGlyMetLysThrArgIleArgMetGlyGlnTyr	280
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Qy	281	GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn	300
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Qy	301	LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp	320
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Qy	341	AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg	360
Db	1088	GACAAAGACCACTGGGACGAAGTCAAGGAGAGATGACCAGTGCCCTTGGCCACTATGCGG	1147
Qy	361	ValAspTyrGluGlnIleLysIleLysIleGluAspAlaSerAsnProLeuLeuLeu	380
Db	1148	GTAGACTACGACCAAGGTGAAGATCAAGGACCTGAAGACCTCTAACACCGGCTCCTCAAC	1207
Qy	381	LysArgArgLysLysAlaArgAlaLeuGluAlaAlaAla	393
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; Sequence 2938, Application US/10488619			
; Publication No. US20060099578A1			
; GENERAL INFORMATION:			
; APPLICANT: Greenlee, Winner and Sullivan, P.C.			
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations			
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays			
; FILE REFERENCE: 98-01 WO			
; CURRENT APPLICATION NUMBER: US/10/488,619			
; NUMBER OF SEQ ID NOS: 3040			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 2938			
; LENGTH: 574			
; TYPE: DNA			
; ORGANISM: Mus musculus			
US-10-488-619-2938			
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Best Local Similarity:	98.1%	Mismatches:	1

Query Match:	37.9%	Indels:	0
DB:	6	Gaps:	0
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Qy	262	AsnHisGlyLeuAlaileSerProGlyMetLysThrArgIleArgMetGlyGlnTyrGlu	281
Db	61	AATCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGTATTCGAATGGGCCAGTATGAA	120
Qy	282	PheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsnLeu	301
Db	121	TTTCCTTAACCCGGATTGGTCAGAAGTATCAGAAGAAAGTGAAGATGCTTATCCGGAATCTG	180
Qy	302	LeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrpIle	321
Db	181	CTAAAAACAGAGCCCCACCCAGAGAATGACCATCACAGAAATTCATGAACCCCTGGATC	240
Qy	322	MetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGluAsp	341
Db	241	ATGCAATCTACGAAGGTCCCTCAGACTCCACTGCACACCAGCGGTGTCTGAAGGAGGAC	300
Qy	342	LysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArgVal	361
Db	301	AAGGAACGATGGGAGGATGTCAAGGAGGAGATGACCAGTGCCCTTGGCCACGATGCGTGT	360
Qy	362	AspTyrGluGlnIleLysIleLysIleGluAspAlaSerAsnProLeuLeuLys	381
Db	361	GACTATGAGCAGATCAAGATAAAGAAGATAGAAGACGCATCCCAACCCCTCTGCTTCTCAAG	420
Qy	382	ArgArgLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis	396
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US-11-242-505A-40			
; Sequence 40, Application US/11242505A			
; Publication No. US20060099656A1			
; GENERAL INFORMATION:			
; APPLICANT: Carroll, Joseph M.			
; APPLICANT: Healy, Aileen			
; TITLE OF INVENTION: Methods and Compositions for Treating			
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,			
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,			
; FILE REFERENCE: MPI2001-288P1RCPIONMIM			
; CURRENT APPLICATION NUMBER: US/11/242,505A			
; CURRENT FILING DATE: 2005-10-03			
; PRIOR APPLICATION NUMBER: US 10/290,078			
; PRIOR FILING DATE: 2002-11-07			
; PRIOR APPLICATION NUMBER: US 60/347,949			
; PRIOR FILING DATE: 2001-11-07			
; PRIOR APPLICATION NUMBER: US 10/320,351			
; PRIOR FILING DATE: 2002-12-16			
; PRIOR APPLICATION NUMBER: 60/341,606			
; PRIOR FILING DATE: 2001-12-17			
; NUMBER OF SEQ ID NOS: 48			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO 40			
; LENGTH: 1740			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-11-242-505A-40			
Alignment Scores:			
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Score:	522.00	Matches:	119
Percent Similarity:	56.3%	Conservative:	55
Best Local Similarity:	38.5%	Mismatches:	117
Query Match:	24.8%	Indels:	19
DB:	7	Gaps:	7


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US-10-469-221-2 (1-396) x US-11-242-505A-40 (1-1740)
QY 16 ProProGlnProProThrProAlaLeuProHisProProAlaGlnProProProProPro 35
Db 97 CCTCCTGCTCCGCCTCGTCTCTTCGGTCCGCCAGTGC GGCCCGGGACCGCGA 156
QY 36 ProGlnGlnPheProGlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIle 55
Db 157 GCCTCGTCC-----CGGATTACTGGATCGACGGCTCC-AACAGGGATGCGCTG 203
QY 56 IleAspAspTyrLysValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeu 75
Db 204 AGCGATTCTTCGAGTGGAGTCGGAG---CTGGACGGGTGCTACATCCATTGTGTAC 260
QY 76 GlnIlePheAsnLysArgThrGlnGluLysPheAlaLeuLysMetLeuGln----- 92
Db 261 AGATGCAAAACAGAGGGGCCCTTATGCTCTCAAAGTGTAAAGAAACAGTG 320
QY 93 AspCysProLysAlaArgGluValGluLeuHisTrpArgAlaSerGlnCysProHis 112
Db 321 GACAAAAAATCGTAAGAACTGAGATAGGAGTCTTCTTCGCCTCTCACAT---CCAAAC 377
QY 113 IleValArgIleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCysLeuLeuIle 132
Db 378 ATTATAAAACTTAAAGAGATATTGTGAAACCCCTACAGAA-----ATCAGTCTG 425
QY 133 ValMetGluCysLeuAspGlyGlyLeuPheSerArgIleGlnAspArgGlyAspGln 152
Db 426 GTCCTAGAACTCGTCACAGGAGGAACTGTTTGATAGGATTGTGGAAAGGGA----- 479
QY 153 AlaPheThrGluArgGluAlaSerGluIleMetLysSerIleGlyGluAlaIleGlnTyr 172
Db 480 TATTACAGTGAGCGAGATGCTGCAGATGCCGTAAACAAATCCTGGAGGCAGTGTAT 539
QY 173 LeuHisSerIleAsnIleAlaHisArgAspValLysProGluAsnLeuTyrThrSer 192
Db 540 CTACATGAAAAATGGGATTGTCCATCGTATCTCAAACCAGAGAATCTTTTATGCAACT 599
QY 193 LysArgProAsnAlaIleLeuLysLeuThrAspPheGlyPheAlaLysGluThrThrSer 212
Db 600 CCAGCCCCAGATGACCACTCAAATCGCTGATTTGGACTCTCTAAATTTGTGGAACAT 659
QY 213 HisAsnSerLeuThrThrProCysTyrThrProTyrTyrValAlaProGluValLeuGly 232
Db 660 CAAGTGCTCATGAGACAGATATGTGGAACCCAGGGTACTGCGCACCTGAAATCTTAGA 719
QY 233 ProGluLysTyrAspLysSerCysAspMetTrpSerLeuGlyValIleMetTyrIleLeu 252
Db 720 GGTGTGCTATGGACCTGAGGTGGACATGTGGTCTGTAGGAATAATCACCTACATCTTA 779
QY 253 LeuCysGlyTyrProPheTyrSerAsnHisGlyLeuAlaIleSerProGlyMetLys 272
Db 780 CTTTGTGGATTGTAACCATCTCTATGATGAAAGAGGC-----GATCAGTTCATGTTT 830
QY 273 ThrArgIleArgMetGlyGlnTyrGluPheProAsnProGluTyrSerGluValSerGlu 292
Db 831 AGGAGAATCTCGAATTGTGAATATTACTTTATCTCCCTGGTGGGATGAAGTATCTCTA 890
QY 293 GluValLysMetLeuIleArgAsnLeuLysThrGluProThrGlnArgMetThrIle 312
Db 891 AATGCCAAGGACTTGGTCAGAAAAATTAATTTTGGATCCAAAGAAACCGCTGACTACA 950
QY 313 ThrGluPheMetAsnHisProTrpIle 321
Db 951 TTTCAAGCTCTCCAGCATCCGTGGGTC 977
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RESULT 6

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US-11-242-505A-41
; Sequence 41, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; FILE REFERENCE: MPI2001-288P1RCP1OMNIM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (78) ... (1499)
US-11-242-505A-41
Alignment Scores:
Pred. No.: 8.8e-30 Length: 1740
Score: 522.00 Matches: 119
Percent Similarity: 56.3% Conservative: 55
Best Local Similarity: 38.5% Mismatches: 117
Query Match: 24.8% Indels: 19
DB: 7 Gaps: 7
US-10-469-221-2 (1-396) x US-11-242-505A-41 (1-1740)
QY 16 ProProGlnProProThrProAlaLeuProHisProProAlaGlnProProProProPro 35
Db 97 CCTCCTGCTCCGCCTCGTCTCTTCGGTCCGCCAGTGC GGCCCGGGACCGCGA 156
QY 36 ProGlnGlnPheProGlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIle 55
Db 157 GCCTCGTCC-----CGGATTACTGGATCGACGGCTCC-AACAGGGATGCGCTG 203
QY 56 IleAspAspTyrLysValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeu 75
Db 204 AGCGATTCTTCGAGTGGAGTCGGAG---CTGGACGGGTGCTACATCCATTGTGTAC 260
QY 76 GlnIlePheAsnLysArgThrGlnGluLysPheAlaLeuLysMetLeuGln----- 92
Db 261 AGATGCAAAACAGAGGGGCCCTTATGCTCTCAAAGTGTAAAGAAACAGTG 320
QY 93 AspCysProLysAlaArgGluValGluLeuHisTrpArgAlaSerGlnCysProHis 112
Db 321 GACAAAAAATCGTAAGAACTGAGATAGGAGTCTTCTTCGCCTCTCACAT---CCAAAC 377
QY 113 IleValArgIleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCysLeuLeuIle 132
Db 378 ATTATAAAACTTAAAGAGATATTGTGAAACCCCTACAGAA-----ATCAGTCTG 425
QY 133 ValMetGluCysLeuAspGlyGlyLeuPheSerArgIleGlnAspArgGlyAspGln 152
Db 426 GTCCCTAGAACTCGTCACAGGAGGAACTGTTTGATAGGATTGTGGAAAGGGA----- 479
QY 153 AlaPheThrGluArgGluAlaSerGluIleMetLysSerIleGlyGluAlaIleGlnTyr 172
Db 480 TATTACAGTGAGCGAGATGCTGCAGATGCCGTAAACAAATCCTGGAGGCAGTGTAT 539
QY 173 LeuHisSerIleAsnIleAlaHisArgAspValLysProGluAsnLeuTyrThrSer 192
Db 540 CTACATGAAAAATGGGATTGTCCATCGTATCTCAAACCAGAGAATCTTTTATGCAACT 599
QY 193 LysArgProAsnAlaIleLeuLysLeuThrAspPheGlyPheAlaLysGluThrThrSer 212
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Db      600 CCAGCCCCAGATGCACCACTCAAAATCGCTGATTTTGGACTCTCTAAAAATTGTGGAACAT 659
QY      213 HisAsnSerLeuThrThrProCysTyrThrProTyrTyrValAlaProGluValLeuGly 232
Db      660 CAAGTGCTCATGAAGACAGTATGTGGAACCCAGGGTACTGCGCACCTGAAATTTCTTAGA 719
QY      233 ProGluLysTyrAspLysSerCysAspMetTrpSerLeuGlyValIleMetTyrIleLeu 252
Db      720 GGTGTGCCTATGCACCTGAGGTGGACATGTGGTCTGTAGGAATATACCTACATCTTA 779
QY      253 LeuCysGlyTyrProProPheTyrSerAsnHisGlyLeuAlaIleSerProGlyMetLys 272
Db      780 CTTTGTGGATTGGAACCATTTCTATGATGAAAGAGGC-----GATCAGTTTCATGTTT 830
QY      273 ThrArgIleArgMetGlyGlnTyrGluPheProAsnProGluTrpSerGluValSerGlu 292
Db      831 AGGAGAAATCTGAATTGTGAATATTACTTTATCTCCCCCTGGTGGGATGAAGTATCTCTA 890
QY      293 GluValLysMetLeuIleArgAsnLeuLysThrGluProThrGlnArgMetThrIle 312
Db      891 AATGCCAAGGACTTGGTCAGAAAATTAAATTTTGGATCCAAAGAAACGGCTGACTACA 950
QY      313 ThrGluPheMetAsnHisProTirIle 321
Db      951 TTTCAAGCTCTCCAGCATCCGTGGGTC 977
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RESULT 7

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US-10-449-902-20013
; Sequence 20013, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20013
; LENGTH: 1937
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK070346
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-20013
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Alignment Scores:
Pred. No.: 9.56e-29 Length: 1937
Score: 508.50 Matches: 126
Percent Similarity: 49.6% Conservative: 53
Best Local Similarity: 34.9% Mismatches: 137
Query Match: 24.1% Indels: 45
DB: 6 Gaps: 12

US-10-469-221-2 (1-396) x US-10-449-902-20013 (1-1937)

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QY      1 SerGlnGlyGlnSerPro-----ProValPro 9
Db      45 TCCCAATCCCAATCCCATCCCAACACCAAGCACCACCACCACCAACCAACCCCGG 104
QY      10 PheProAlaProAlaProProGlnProProThrProAlaLeuProHisProProAla 29
Db      105 GCCCCCCAAGCCCCAAGCCCCAAGCCCCAGCCCGCCCG-----CAGCAGCCCGCATCT 158
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QY      30 GlnProProProPro-----ProGlnGlnPhePro---GlnPheHisValLys 45
Db      159 CAGCCTCCGCCCGCCCGGGCACCAAGCCCCAGAGGGCCCCAGAGGGCGGGCGGAG 218
QY      46 SerGlyLeuGlnIleLysLysAsnAlaIleIleAspAspTyrLysValThr-----62
Db      219 GATGGGTGGGGCGGGTGTCTGGGGCGGCCCATGGAGGACGTCCGTGCGACCTACACCTTC 278
QY      63 SerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLysArgThr 82
Db      279 GGGCGGAGCTGGGGCGGGGCGAGTTCGGGGGTGACCTACCTCGCCACCCACAAGCCACC 338
QY      83 GlnGluLysPheAlaLeuLysMetLeu-----GlnAspCys 94
Db      339 GGCCGACGCTACGCTGCAAGTCCATCGCCGCCGCCGCAAGCTCGCCGCCCGACGACCTC 398
QY      95 ProLysAlaArgArgGluValGluLeuHisTrpArgAlaSerGlnCysProHisIleVal 114
Db      399 GACGACGTCGCCCGCGAGGTCACATCATGACCACTCACCGGCCACCGCAACATCGTC 458
QY      115 ArgIleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMet 134
Db      459 GAGCTGCGCGCGCCTACGAGGAC-----CGCCACTCCGTCAACCTCGTCATG 506
QY      135 GluCysLeuAspGlyGlyGluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPhe 154
Db      507 GAGCTCTCGAGGGCGCGAGCTCTTCGACCGCATCATCGCCAGGGGCCAC-----TAC 560
QY      155 ThrGluArgGluAlaSerGluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHis 174
Db      561 TCCGAGCGCGCGCCGCCCTCTGCGAGGAGATCGTCTCCGTCTTCTCAAGCCCGGTGAG 620
QY      175 SerIleAsnIleAlaHisArgAspValLysProGluAsnLeuTyrThrSerLysArg 194
Db      621 TCCATGGGGTCAATGCACAGGGACCTCAAGCCCGAGAACTTCCTCTCTCTCAACAAGCGC 680
QY      195 ProAsnAlaIleLeuLysLeuThrAspPheGly-----PheAlaLysGluThrThr 211
Db      681 GAGGACTCCCGCTCAAAGCCACCGAATTTGGCCTCTCCGTCTTCTCAAGCCCGGTGAG 740
QY      212 SerHisAsnSerLeuThrThrProCysTyrThrProTyrTyrValAlaProGluValLeu 231
Db      741 CAGTTCAAGATCTTGTGGA-----AGTGCAATATTATGTGGCTCTTGAGGTCTTA 791
QY      232 GlyProGluLysTyrAspLysSerCysAspMetTrpSerLeuGlyValIleMetTyrIle 251
Db      792 ---AAACGACTATATGGAGCTGAGGCAGACATATGGAGTGTGGAGTTATCCTTTACATC 848
QY      252 LeuLeuCysGlyTyrProProPheTyrSerAsnHisGlyLeuAlaIleSerProGlyMet 271
Db      849 CTTCTATCAGGGGTTCTCCATTCTGGGCAGAAAAAC-----GAGGACGGTATA 896
QY      272 LysThrArgIleArgMetGlyGlnTyrGluPheProAsnProGluTrpSerGluValSer 291
Db      897 TTTGATGCTGTTCTGCAAGGTCAATATCGACTTCTCATCTGAACCATGGCCTTCTATATCT 956
QY      292 GluGluValLysMetLeuIleArgAsnLeuLeuLysThrGluProThrGlnArgMetThr 311
Db      957 AGTGGTGCAAAAGACTTGGTCAAGCGGATGCTTCGGCAGGACCCCAAGGAGCGGTAACT 1016
QY      312 IleThrGluPheMetAsnHisProTirIleMetGlnSerThrLysValProGlnThrPro 331
Db      1017 GCTGCTGAATTTTGAACCCCATGGATTAGAGAGGATGGAGAGGGCCCCAGATAAACCA 1076
QY      332 Leu 332
Db      1077 CTT 1079
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RESULT 8

US-10-449-902-21986
; Sequence 21986, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21986
; LENGTH: 2641
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK072204
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-21986

Alignment Scores:
Pred. No.: 9 41e-28 Length: 2641
Score: 497.00 Matches: 132
Percent Similarity: 48.8% Conservative: 70
Best Local Similarity: 31.9% Mismatches: 152
Query Match: 23.6% Indels: 61
DB: 6 Gaps: 13

US-10-469-221-2 (1-396) x US-10-449-902-21986 (1-2641)

QY 5 SerProProValProPhe-----ProAlaProAlaProProGln----- 18
Db 821 AGCCCCCGAGCAGCTCAAGATCGTCTCGACCACGGACACCGCCTCCGCCGAGCAGCG 880

QY 19 ProProThrProAlaLeuProHisProProAlaGlnProProProProProGlnGln 38
Db 881 CCTCCAAGTCGAGCGCGGCTCGGACTCCGGCGAGGCCGCCAGG-CCGCGCGGAGGGTG 939

QY 39 PheProGlnPheHisValLysSerGly-----LeuGlnIleLys 51
Db 940 CCGCCGGTGAAAGCGGTCTCCAGCGCGGGGTCTCGTCTGGTCTCGTGAAGCGCAAG 999

QY 52 LysAsnAlaIleleAaspTyrLysValThrSerGlnValLeuGlyLeuGlyIleAsn 71
Db 1000 ACGGAGAGTCTCAAGACAAGTACAGCCTG---GGCGGAAGTCTCGGCGAGGGCAGTTC 1056

QY 72 GlyLysValLeuGlnIlePheAsnLysArgThrGlnGluLysPheAlaLeuLysMetLeu 91
Db 1057 GGGACGACGTACCTGCTGCTGGAGCGCGCCACCGCAAGGAGTTCGCCTGCAAGTCCATC 1116

QY 92 -----GlnAspCysProLysAlaArgArgGluValGluLeu 103
Db 1117 CTGAAGCGGAAGCTGGTCAACCGACGACGCTCGAGGACGTCCGCCGCGAGATCCAGATA 1176

QY 104 HisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyrGluAsnLeu 123
Db 1177 ATGTACCACCTCGCCGGCCACCCCAACGTGATCTCCATCAGGGGGCGCTACGAGGACGCC 1236

QY 124 TyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGlyGluLeuPhe 143
Db 1237 GTCGCC-----GTGCACCTCGTCAATGAGAGTCTGCGCCGCGCGGAGCTGTTC 1284

QY 144 SerArgileGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMet 163
Db 1285 GACCGGATCGTCCAGAAGGGGCAC-----TACACCGAGCGGAAGCGCGGAGCTCGCC 1338

QY 164 LysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHisArgAspVal 183
Db 1339 AGGGTCATCGTCGGCGTCTGTCGAGGTGTGCCACTCCATGGGCGTGATGCACCGTGATCTC 1398

QY 184 LysProGluAsnLeuTyrThrSerLysArgProAsnAlaIleLeuLysLeuThrAsp 203
Db 1399 AAGCCCGAGAACTTCTCTTCGCCGACACAGAGGAGGCGCTCTCAAGACCATTGAC 1458

QY 204 PheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCysTyrThrPro 223
Db 1459 TTTGGTCTCTCCATTTCTTTTCGCCCCAGGTCAAGTATTCACTGATGTTGTTGGTAGCCCT 1518

QY 224 TyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCysAspMetTyr 243
Db 1519 TACTATGTCGCCGAGAGTTCTG---AAAAAGAAATATGGTCAAGAGGACAGATGCTGG 1575

QY 244 SerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyrSerAsnHis 263
Db 1576 AGCGCTGGTGTGATAATTTACATCTTGTGTGGTGTGCCGCCCATTTGGGCAGAGAAC 1635

QY 264 GlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyrGluPhePro 283
Db 1636 -----GAGCAGGGTATATTTGAAGAGGGTTTTCATGGTAGACTTTCAG 1683

QY 284 AsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsnLeuLys 303
Db 1684 TCAGAACCATGGCCTAGCATCTCTGAAGGTGCCAAAGATCTCGTAAGGAGAATGCTTGT 1743

QY 304 ThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrpIleMetGln 323
Db 1744 AGGGACCCGGAAGAGATTGACAGCTCATGAAGTTTAAAGGCATCCATGGTCCAGGTT 1803

QY 324 SerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGluAspLysGlu 343
Db 1804 GGTGGTTTGGCTCCTGACAAGCCCTG---GATTCTGCTGTTCTATCTCGTATGAAGCAA 1860

QY 344 -----ArgTrpGluAspValLys 349
Db 1861 TTCTCAGCTATGAATAAGCTGAAAAAGATGGCTCTTAGGGTCATTGCAGAGAACCTATCT 1920

QY 350 GluGluMetThrSerAlaLeuAlaThrMet----- 359
Db 1921 GAAGACGAAATCGCCGCCCTGAAAGAAATGTTCAAGATGATCGACACAGACAACAGTGGA 1980

QY 360 ArgValAspTyrGluGlnIleLysIle-----LysLysIle 371
Db 1981 CAGATCACCTTCGAAGAACTCAAGGTTGGTCTGAAAAAAGTC 2022

RESULT 9
US-10-449-902-26866
; Sequence 26866, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26866
; LENGTH: 2524
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK102308
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-26866

Alignment Scores:

Pred. No.:	1.3e-26	Length:	2524
Score:	481.00	Matches:	116
Percent Similarity:	50.9%	Conservative:	57
Best Local Similarity:	34.1%	Mismatches:	123
Query Match:	22.8%	Indels:	44
DB:	6	Gaps:	8
US-10-469-221-2 (1-396) x US-10-449-902-26866 (1-2524)			
Qy	24	LeuProHisProProAlaGlnProProPro-----	33
Db	647	CTGGGTCCGCGCCAAATGCAGCCGACCCGAGCGGGAGCGGACGAAACGCCAAT	706
Qy	34	-----ProProProGlnGlnPheProGlnPheHisValLysSerGly	47
Db	707	GCGAAGCGAAGCTGGCGCGCGCGTGTACGGCGGGAGTCTGGCGGTCTCGGTG	766
Qy	48	LeuGlnIleLysLysAsnAlaIleIleAspAspTyrLysValThrSerGlnValLeuGly	67
Db	767	CTGCCGCAAGACGGCGAACGTGCGGACCACTACCGCATC---GGGAAGAAGCTCGGG	823
Qy	68	LeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLysArgThrGlnGluLysPheAla	87
Db	824	CAGGGGCAGTTCGGGACGACGTACCTGTGCGTGGACAAGCGGAGCGCGGAGTTCGCG	883
Qy	88	LeuLysMetLeu-----GlnAspCysProLysAlaArgArg	99
Db	884	TGCAAGTCCATCCCCAAGCGGAAGCTGCTGTGCCGGGAGGACTACGAGGACGTGTGGCGC	943
Qy	100	GluValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspVal	119
Db	944	GAGATCCAGATCATGCACCACCTCTCCGAGCACCCCAACGTCTGCGCATCCGCGCGCC	1003
Qy	120	TyrGluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGly	139
Db	1004	TACGAGGACGCGCTG-----TTCGTCCACATCGTCAATGAGCTCTGCGCGCGC	1051
Qy	140	GlyGluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAla	159
Db	1052	GGCGAGCTCTCGACCGCATCGTCGCCAAGGGCCAC-----TACACCGAGCGCGCGCC	1105
Qy	160	SerGluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAla	179
Db	1106	GCGCAGCTCATCGCACCATCGTCGCCGCTCGTCGAGGATGCCACTCGCTCGGCGTCAATG	1165
Qy	180	HisArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeu	199
Db	1166	CACCGGGACCTCAAGCCCGAGAACTCTCTTCGCCAGCGCGCGGAGGACGCCCCCTC	1225
Qy	200	LysLeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrPro	219
Db	1226	AAGGCCACTGATTTCCGCCTCTCCATGTTCTACAAGCCTGGTGATAAGTTCTCTGATGT	1285
Qy	220	CysTyrThrProTyrTyrValAlaProGluValLeu-----GlyProGluLys	235
Db	1286	GTTGGGAGCCCTATTATGTTGCACCTGAGGTACTTCAGAAATGCTATGGTCCAGAACT	1345
Qy	236	TyrAspLysSerCysAspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGly	255
Db	1346	-----GATGCTCGAGTGTGGGTAATTCTTTACATTTGCTATGTGT	1390
Qy	256	TyrProProPheTyrSerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIle	275
Db	1391	GTTCCACCATTTTGGGCAGAA-----ACTGAAGCTGGAATTTTCAGGCAGATT	1438
Qy	276	ArgMetGlyGlnTyrGluPheProAsnProGluTyrSerGluValSerGluGluValLys	295
Db	1439	CTACGAGGCAAACTTGATTTTGAATCTGAACCTGGCCTAGCATCTCTGACAGTGTAAA	1498
Qy	296	MetLeuIleArgAsnLeuLysThrGluProThrGlnArgMetThrIleThrGluPhe	315
Db	1499	GATCTAGTCCGTAATATGCTTTTGGCGGGATCTCTACAAAGAGACTTACAGCCCATGAGGT	1558

Qy	316	MetAsnHisProTrpIleMetGlnSerThrLysValProGlnThrProLeuHisThrSer	335
Db	1559	CTCTGTCATCCATGGATTGTTGATGATGCTGTGGCACCTGACAAGCCTATTGATTCTGCT	1618
RESULT 10			
US-10-505-928-350			
; Sequence 350, Application US/10505928			
; Publication No. US20060088532A1			
; GENERAL INFORMATION:			
; APPLICANT: Ludwig Institute for Cancer Research et al.			
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES			
; FILE REFERENCE: 28967/39178			
; CURRENT APPLICATION NUMBER: US/10/505,928			
; CURRENT FILING DATE: 2004-08-27			
; PRIOR APPLICATION NUMBER: US 60/363,019			
; PRIOR FILING DATE: 2002-03-07			
; NUMBER OF SEQ ID NOS: 866			
; SOFTWARE: PatentIn 3.2			
; SEQ ID NO 350			
; LENGTH: 3982			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-505-928-350			
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Qy	31	-----ProProProProProGlnGlnPhe-----ProGlnPheHisVal	44
Db	1401	CTGCACAAAGTCCCAGTTTCAACCAATCGTGCAGCAGTTACACGGGAACAACATCCACTTC	1460
Qy	45	LysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspAspTyrLysValThrSerGln	64
Db	1461	ACCGATGGCTACGAGATCAAGGAGGACATCGGGTGGGCTCTACTCAGTGTGCAAGCGA	1520
Qy	65	ValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLysArgThrGlnGlu	84
Db	1521	TGTGTG-----CATAAAGCCACAGACACC	1544
Qy	85	LysPheAlaLeuLysMetLeuGlnAspCysProLysAlaArgArg-----Glu	100
Db	1545	GAGTATGCGGTGAAGATCATTGAT-----AAGAGCAAGAGAGACCCCTCGGAAGAG	1595
Qy	101	ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr	120
Db	1596	ATTGAGATCCTCTCGGTTACGGCCAGCACCCGAACATCATCACCCCTCAAGGATGCTAT	1655
Qy	121	GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly	140
Db	1656	GATGAT-----GGCAAGTTGTGTACCTGGTAATGGAGTGTGTCGTGGTGGG	1703
Qy	141	GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer	160
Db	1704	GAGCTCCTGGACCGCATCTCTCCGGCAG-----AGATACTTCTCGAGCGCGAAGCCAGT	1757
Qy	161	GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis	180
Db	1758	GACGTCTCTGTGCACCATCACCAAGACCATGGACTACCTCCATTCACAGGGGGTGTGTTCAT	1817

Db 303 GGCCAGTTTGGTGTACGCFACCTCGTAACTCACAAGAGACGAAACAACAGGTCGCTTGC 362

QY 89 LysMetLeu-----GlnAspCysProLysAlaArgArgGlu 100
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363 AAGTCAATCCCTACGCGCGCCTTGTTCAAAAGACGACATGAAGATGTCGCGTGAA 422

QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValaspValTyr 120
|||:::
Db 423 GTCCAGATTATGCACCATCTCAGCGGTCAACCGGAACATAGTGGACTTGAAGGGAGCCTAC 482

QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
|||:::
Db 483 GAGGAC-----AGACACTCTGTGAATCTGATAATGGAGTTGTGTGAAGGAGGG 530

QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
|||:::
Db 531 GAATTGTTTCGATAGGATCATTTCTAAAGGT-----CTTTACTCAGAGAGGCTGCTGCG 584

QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
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Db 585 GATTTGTGTAGGCAGATGGTGTATGGTGTGCATAGTTGTCTATTCTATGGTGTAAATGCAC 644

QY 181 ArgAspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLys 200
|||:::
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QY 201 LeuThrAspPheGly-----PheAlaLysGluThrThrSerHisAsnSerLeuThr 217
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Db 705 GCTACAGACTTTGGTCTCTCTGTCTCTTCAAGCCAGGTGATAAGTTTAAGGATCTTGTT 764

QY 218 ThrProCysTyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAsp 237
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Db 765 GGA-----AGTGCACTACTATGTTGCCCCAGAACTCTA---AAACGGAACTATGGA 812

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Db 813 CCAGAGGCTGATATCTGGAGTGTGGTGTGATTCTATACATCCTTCTCAGTGGTGTCCG 872

QY 258 ProPheTyrSerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMet 277
|||:::
Db 873 CCTTCTGGGGAGAAAAT-----GAAACGGGGATCTTTGATGCCATCTTCAA 920

QY 278 GlyGlnTyrGluPheProAsnProGluTyrSerGluValSerGluGluValLysMetLeu 297
|||:::
Db 921 GGGCAACTTGATTTTTCAGCTGATCCATGGCCAGCACTATCAGATGGTGGCCAAAGATCTT 980

QY 298 IleArgAsnLeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsn 317
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Db 981 GTGAGGAAAATGTTAAATATGACCCCTAAAGATCGGCTTACAGCTGCGGAAGTGCTAAAT 1040

QY 318 HisProTrpIleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgVal 337
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Db 1041 CATCCGTGGATTAGAGAAGATGGGAGGCATCAGACAAACCGCTTGACAAATGCG---GTG 1097

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Db 1098 TTATCCAGGATGAACAACAAATTCGGGCGATGAACAACATAAAAAAATGGCCCTGAAGGTT 1157

QY 356 LeuAlaThrMetArgValaspTyrGluGlnIleLysIleLysLysIle 371
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 19, 2006, 15:08:32 ; Search time 235 Seconds
(without alignments)
4729.526 Million cell updates/sec

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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2078	98.7	1336	3	US-09-023-655-1397 Sequence 1397, Ap
2	1991.5	94.6	2258	3	US-09-016-434-1415 Sequence 1415, Ap
3	1391	66.0	2481	3	US-09-016-434-1088 Sequence 1088, Ap
4	1391	66.0	2482	3	US-09-949-016-5682 Sequence 5682, Ap
5	1391	66.0	2509	3	US-09-949-016-660 Sequence 660, App
6	1333	63.3	1333	3	US-09-142-551A-1 Sequence 1, Appli
7	540	25.6	3061	4	US-09-880-107-2146 Sequence 2146, Ap
8	536	25.5	1671	3	US-09-733-388-5 Sequence 5, Appli

9	536	25.5	1671	3	US-10-446-175-5	Sequence 5, Appli
10	532.5	25.3	1733	3	US-09-620-312D-526	Sequence 526, App
11	529.5	25.1	1694	3	US-09-579-664B-3	Sequence 3, Appli
12	529.5	25.1	1694	3	US-10-355-975A-3	Sequence 3, Appli
13	529.5	25.1	1694	5	US-09-980-464-3	Sequence 3, Appli
14	523	24.8	1442	3	US-09-949-016-1590	Sequence 1590, Ap
15	523	24.8	1442	3	US-09-949-016-1591	Sequence 1591, Ap
16	523	24.8	1480	3	US-09-016-434-1454	Sequence 1454, Ap
17	498	23.6	2447	3	US-09-960-643-1	Sequence 1, Appli
18	496.5	23.6	1074	3	US-09-733-388-3	Sequence 3, Appli
19	496.5	23.6	1074	3	US-10-446-175-3	Sequence 3, Appli
20	496.5	23.6	1158	3	US-09-733-388-1	Sequence 1, Appli
21	496.5	23.6	1158	3	US-10-446-175-1	Sequence 1, Appli
22	486	23.1	1584	3	US-09-799-451-205	Sequence 205, App
23	484.5	23.0	2165	3	US-09-620-312D-809	Sequence 809, App
24	484.5	23.0	3471	2	US-08-715-568A-2	Sequence 2, Appli
25	474.5	22.5	1458	3	US-09-230-896C-5	Sequence 5, Appli
26	467	22.2	3119	3	US-09-949-016-1939	Sequence 1939, Ap
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28	464.5	22.1	2061	3	US-10-096-960-1	Sequence 1, Appli
29	454.5	21.6	1282	2	US-08-878-989-12	Sequence 12, Appl
30	454.5	21.6	1282	3	US-09-272-796-12	Sequence 12, Appl
31	454.5	21.6	1282	3	US-09-016-434-953	Sequence 953, App
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33	443	21.0	1545	3	US-10-620-845-1	Sequence 1, Appli
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37	443	21.0	2287	3	US-10-104-047-1539	Sequence 1539, Ap
38	441	20.9	1735	3	US-09-746-694-3	Sequence 3, Appli
39	441	20.9	1858	3	US-09-529-093A-1	Sequence 1, Appli
40	441	20.9	1858	3	US-09-529-154-1	Sequence 1, Appli
41	441	20.9	1858	3	US-10-185-182A-1	Sequence 1, Appli
42	440.5	20.9	1991	3	US-10-104-047-1214	Sequence 1214, Ap
43	438	20.8	2230	3	US-09-828-313-26	Sequence 26, Appl
44	435.5	20.7	2298	3	US-09-975-326-3	Sequence 3, Appli
45	435.5	20.7	2298	3	US-10-217-357-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-09-023-655-1397
; Sequence 1397, Application US/09023655
; Patent No.6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

```
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1397:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9407074
US-09-023-655-1397

Alignment Scores:
Pred. No.:          9.88e-186      Length:      1336
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Query Match:       98.7%          Indels:       0
DB:                3              Gaps:         0

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QY     61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
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QY    101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
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Db    301 GTGGAGCTGCACTGGCGGGCCTCCCAGTGCCTCCCGACATCGTACGGATCGTGGATGTGTAC 360

QY    121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
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Db    361 GAGAACTGTGTACGAGGGAGGAAGTGCCCTGCTGATTGTCATGGAATGTTTGGACGGTGGGA 420

QY    141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
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QY    161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
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Db    541 CGGGATGTCAAGCTGAGAAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCTCTGAAA 600

QY    201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
      |||
Db    601 CTCACCTGACTTTGGCTTTGCCAAGGAAACCACGACCACAACCTCTTTGACCACTCTTGT 660

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Db      661 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGGTCCAGAGAAGTATGACAAAGTCCTGT 720

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Db     721 GACATGTTGGTCTCTGGGTGTCATCATGTACATTCTGCTGTGTGGGTATCCCCCTTCTAC 780

QY     261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
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Db     781 TCCAACCACGCGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840

QY     281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
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Db     841 GAATTTCCCAACCAGAAATGGTCAAGATATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900

QY     301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTyr 320
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Db     901 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCCGAGTTTATGAACCACTTGG 960

QY     321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
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QY     341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360
      |||
Db    1021 GACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCAGTGCCTTGGCCACAATGCGC 1080

QY     361 ValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeu 380
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Db    1081 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAAACCTCTGTGCTGTG 1140

QY     381 LysArgArgLysLysAlaArgAlaLeuGluAlaAlaAlaLeuAlaHis 396
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Db    1141 AAGAGGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCAAC 1188

RESULT 2
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; Sequence 1415, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1415:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 2258 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g530089
US-09-016-434-1415

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Score: 1991.50 Matches: 396
Percent Similarity: 69.0% Conservative: 0
Best Local Similarity: 69.0% Mismatches: 0
Query Match: 94.6% Indels: 178
DB: 3 Gaps: 1

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QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspTyrLys 60
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QY 61 ValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLys 80
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QY 101 ValGluLeuHisTrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyr 120
Db 691 GTGGAGCTGCAGTGGCGGGCTCCCGAGTGCAGCACATCGTACGGATCGTGGATGTGTAC 750

QY 121 GluAsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGly 140
Db 751 GAGAAATCTGTACGAGGGAGGAAGTGCCTGCTGATTTGCATGGAAATGTTGGACGGTGA 810

QY 141 GluLeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSer 160
Db 811 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACGAGGCATTCACAGAAAGAGAGCATCC 870

QY 161 GluIleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHis 180
Db 871 GAAATCATGAAGACATCGGTGAGGCCATCCAGTATCTGCATTTCAATCAACATTTGCCAT 930

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QY 201 LeuThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCys 220
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QY 221 TyrThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCys 240
Db 1051 TATACACCGTACTATGTGGCTCCAGAAGTGTGGGTCCAGAGAAGTATGACAAGTCTGT 1110

QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProPropheTyr 260
Db 1111 GACATGTGGTCCCTGGGTGTTCATCATGTATCATCTGTGTGTGGGTATCCCGCTTCTAC 1170

QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280

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Db 1171 TCCAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGCCAGTAT 1230
QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 1231 GAATTTCCCAACCCAGAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 1291 CTGCTGAAAAACAGAGCCCAACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCTTGG 1350
QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 1351 ATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCCGCGGTCTCTGAAGGAG 1410
QY 341 AspLysGluArgTrpGluAspValLys----- 349
Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGGTGTCTTCAAGAAACAGCAGCAGGCC 1470
QY 349 ----- 349
Db 1471 ACTTGGCTGACCAGGTTGTGAGCAGAGGATCTGTGTTCTGTGCCAACTCAGTGTGTT 1530
QY 349 ----- 349
Db 1531 TCTTAGAATCCTTTTATTCCCTGGGTCTCTAATGGGACCTTAAAGACCATCTGGTATCAT 1590
QY 349 ----- 349
Db 1591 CTTCTCATTTTGCAGAAAGAGAAACTGAGGCCCCAGAGGGCGGAGGTCAGTCTGTCAAGGTC 1650
QY 349 ----- 349
Db 1651 ACGCAGCTGGTGAAGTGGTGGGGCAGACCGGACCCAGGTTTCTGACTCTCTGGCCCCAAGT 1710
QY 349 ----- 349
Db 1711 CTCTTCTCTATCTCTGCGGGATCACTGGGGGGCTCTCAGGGAAACAGCAGAGTGCCATA 1770
QY 349 ----- 349
Db 1771 GCCAGGCTCTGTGTCGCCAGCGCTGGGGTGAGGCTGCCGTTGTGAGCGTGGACCACTAA 1830
QY 349 ----- 349
Db 1831 CCAGCCCCGTCTCTCTCTGTCTGCCACCCCTGCCGCCCTCACCTGCCCTTGTGTCTCTG 1890
QY 349 ----- 349
Db 1891 TCTCTCACTGTCTCTTCTGTGTCTCTCTACTGTCTTCTGGCTCTCTGTACCCCTTCCT 1950
QY 350 -----GluGluMetThrSerAlaLeuAlaThrMetArgValAspTyr 363
Db 1951 GGTGTGCCGTGCCCCCAGGAGGAGATGACCAAGTGCCTTGGCCCAAAATGCGCGTTGACTA 2010
QY 363 rGluGlnIleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLysArgAr 383
Db 2011 CGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACCCCTCTGCTGTGAAGAGCG 2070
QY 383 gLysLysAlaArgAlaLeuGluAlaAlaLeuAlaHis 396
Db 2071 GAAGAAAGCTCGGGCCCTGGAGGCTGGGGCTCGGGCTCTGGCCCCAC 2110

RESULT 3
US-09-016-434-1088
; Sequence 1088, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:

```


Db 647 TATACTCCCTATTATGTGGCCCTTGAGGTCCTGGGTCCAGAGAAGTATGACAAGTCATGT 706
QY 241 AspMetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyr 260
Db 707 GACATGTGGTCCCTGGGTGCATCATGTACATCTCTTTGTGGCTTCCACCCCTTCTAC 766
QY 261 SerAsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyr 280
Db 767 TCCAACACGGGCCAGGCCATCTCCCCGGGATGAAGAGGAGGATTTCGCCTGGGCCAGTAC 826
QY 281 GluPheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsn 300
Db 827 GGCTTCCCCAATCCTGAGTGGTCAGAAGTCTCTGAGGATGCCAAGCAGCTGATCCGCCTC 886
QY 301 LeuLeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrp 320
Db 887 CTGTTGAAGACAGACCCACAGAGAGGCTGACCATCACTCAGTTCAATGAACCAACCCCTGG 946
QY 321 IleMetGlnSerThrLysValProGlnThrProLeuHisThrSerArgValLeuLysGlu 340
Db 947 ATCAACCAATCGATGGACCAAGTCAAGGAGGAGATGACCAGT-----GCCCACTATGCG 1006
QY 341 AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAla-ThrMetAr 360
Db 1007 GACAAAGACCACTGGGACCAAGTCAAGGAGGAGATGACCAGT-----GCCCACTATGCG 1060
QY 360 gValAspTyrGluGlnIleLysIleLysLys-----IleGluAspAlaSerAsnProLe 378
Db 1061 GGTAGACTACGACCAAGTGAAGATCAAGGA-CTTGGCCTGAAGACCTCTTAACAACCGGCT 1119
QY 378 uLeuLeuLysArgArgLysLysAlaArgAlaLeuGluAlaAla 393
Db 1120 CCTCAACAAGAGGAGAGAAAAAAGCAGGCAGGCAGTCTCTGCTCA 1165

RESULT 7

US-09-880-107-2146
; Sequence 2146, Application US/09880107
; Patent No. 6974667
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2146
; LENGTH: 3061
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. 6974667 L07597
US-09-880-107-2146

Alignment Scores:
Pred. No.: 1.22e-40 Length: 3061
Score: 540.00 Matches: 138
Percent Similarity: 52.6% Conservative: 77
Best Local Similarity: 33.7% Mismatches: 139
Query Match: 25.6% Indels: 56
DB: 4 Gaps: 16

US-10-469-221-2 (1-396) x US-09-880-107-2146 (1-3061)

QY 15 ProProGlnProProThrProAlaLeuProHis-----ProProAlaGlnProPro 32

Db 1104 CCGAGTTACGTCCTCCCGCACACCCCAAGGATCCCCCAGGCATCCCCCAGCGCTGGGGCCC 1163
QY 33 -----ProProPro----- 35
Db 1164 ATCAGCTGTCCGGGGCTTCAGCTTCGTGGCCACCGGCTTGATGGAAGACGACGGCAAGC 1223
QY 36 -----ProGlnGlnPheProGlnPheHisValLysSerGlyLeuGlnIleLysLysAsn 53
Db 1224 CTCGTGCCCGG-CAGGCACCCCTGCACTCGGTGGTACAGCAACTCCAT---GGGAAGAAC 1279
QY 54 AlaIleIleAspAspTyrLysValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLys 73
Db 1280 CTGGTTTTTAGTGACGGCTACGTGTGTAAGGAGACAATTGGTGTGGGCTCCTACTCTGAG 1339
QY 74 ValLeuGlnIlePheAsnLysArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAsp 93
Db 1340 TGCAAGCGCTGTGTCCACAAGGCCACCAACATGGAGTATGCTGTCAAGGTCATTGAT--- 1396
QY 94 CysProLysAlaArgArg-----GluValGluLeuHisTrpArgAlaSerGln 109
Db 1397 -----AAGAGCAAGCGGGATCCTTCAGAAGAGATTGAGATTCCTTCGGGTATGGCCAG 1450
QY 110 CysProHisIleValArgIleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCys 129
Db 1451 CACCCCAACATCATCACTCTGAAAGATGTGTATGATGAT-----GGCAAAACAC 1498
QY 130 LeuLeuIleValMetGluCysLeuAspGlyGlyGluLeuPheSerArgIleGlnAspArg 149
Db 1499 GTGTACCTGGTGACAGAGCTGATCGGGGTGGGAGCTGTGGACAAGATCCTGCGGCAG 1558
QY 150 GlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMetLysSerIleGlyGluAla 169
Db 1559 -----AAGTTCTTCTCAGAGCGGGAGGCCAGCTTTGTCTGCACACCATTTGGCAAACT 1612
QY 170 IleGlnTyrLeuHisSerIleAsnIleAlaHisArgAspValLysProGluAsnLeuLeu 189
Db 1613 GTGGAGTATCTGCACCTCACAGGGGGTGTGCACAGGGACCTGAAGCCACGACATCCTG 1672
QY 190 TyrThrSerLysArgProAsn---AlaIleLeuLysLeuThrAspPheGlyPheAlaLys 208
Db 1673 TATGTGGACGAGTCCGGGAATCCCCAGTGCCTGCGCATCTGTGACTTGTGGTTTGCCAA 1732
QY 209 GluThrThrSerHisAsnSer---LeuThrThrProCysTyrThrProTyrTyrValAla 227
Db 1733 CAGCTGGGGCTGAGAATGGGCTCCTCATGACACCTTGCTACACGCCAACTTTGTGGCG 1792
QY 228 ProGluValLeuGlyProGluLysTyrAspLysSerCysAspMetTrpSerLeuGlyVal 247
Db 1793 CCTGAGTGTGAAGCGCCAGGGCTACGATGAAGGCTGCGACATCTGGAGCCTGGGCATT 1852
QY 248 IleMetTyrIleLeuLeuCysGlyTyrProProPheTyrSerAsnHisGlyLeuAlaIle 267
Db 1853 CTGCTGTACACCATGCTGGCAGGATATACTCCATT-----GCCAACGGTCCCAGTGAC 1906
QY 268 SerPro---GlyMetLysThrArgIleArgMetGlyGlnTyrGluPheProAsnProGlu 286
Db 1907 ACACCAGAGGAAATCCTAACCCCGGATCGGCAGTGGGAAGTTTACCCTCAGTGGGGAAAT 1966
QY 287 TrpSerGluValSerGluGluValLysMetLeuIleArgAsnLeuLeuLysThrGluPro 306
Db 1967 TGAACACAGTTTCAGAGACAGCCCAAGGACCTGGTGTCCAAGATGCTACACGTGGATCCC 2026
QY 307 ThrGlnArgMetThrIleThrGluPheMetAsnHisProTrpIleMetGlnSerThrLys 326
Db 2027 CACCAGCGCCTCACAGCTAAGCAGGTCTGCAGCATCCATGGGTCAACCCAGAAAGACAAG 2086
QY 327 ValProGlnThrProLeu---HisThrSerArgValLeuLysGluAspLysGluArgTrp 345
Db 2087 CTTCCCCAAAGCCAGCTGTCCCAACGACCTACAGCTT----- 2125
QY 346 GluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArgValAspTyrGluGln 365

Db 2126 -----GTGAGGAGCCATGGCTGCCACGTACTCCGCACTCAACAGACTCCAAGCCACC 2179

QY 366 IleLysIleLysLysIleGluAspAlaSerAsnProLeuLeuLeuLysArgArgLysLys 385

Db 2180 CCCAGCTGAAGCCCATCGAGTCATCC-----ATCCTGGCCAGCGGCGA----- 2224

QY 386 AlaArgAlaLeuGluAlaAlaAlaLeu 394

Db 2225 GTGAGGAAGTTGCCATCCACCACCCTG 2251

RESULT 8

US-09-733-388-5

; Sequence 5, Application US/09733388

; Patent No. 6602698

; GENERAL INFORMATION:

; APPLICANT: Donoho, Greg

; APPLICANT: Scoville, John

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Abuin, Alejandro

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6602698el Human Kinase Proteins and

; TITLE OF INVENTION: Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0103-USA

; CURRENT APPLICATION NUMBER: US/09/733,388

; CURRENT FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: US 60/169,428

; PRIOR FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 1671

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-733-388-5

Alignment Scores:

Pred. No.:	1,21e-40	Length:	1671
Score:	536.00	Matches:	135
Percent Similarity:	53.0%	Conservative:	75
Best Local Similarity:	34.1%	Mismatches:	145
Query Match:	25.5%	Indels:	41
DB:	3	Gaps:	14

US-10-469-221-2 (1-396) x US-09-733-388-5 (1-1671)

QY 2 GlnGlyGlnSerProProValPro---PheProAlaProAlaProProGlnProPro 20

Db 37 CAGCCCGAGCCCGCGCATCCCCCGCCCTCTGGCCCCGCGCCGCCCGCGGCCCC 96

QY 21 ThrProAlaLeuProHisProProAlaGlnProPro-----Pro 33

Db 97 CTCCCCAGCGCG-----CCCCCGCGCTCTCCGCGCGGGAAGTTGGCGCGCAGCCC 150

QY 34 ProPro-ProGlnGlnPheProGlnPheHisValLysSerGlyLeuGlnIleLysLysAs 53

Db 151 GAGCCGTCGTCGGCCATGGCCCGGAGAACGGCGAGAGCAGTCTCTCTGGAAAAAGCA 210

QY 53 nAlaIleIleAspAspTyrLysValThr-----SerGlnValLeuGlyLeuGlyI1 70

Db 211 AGCT-----GAAGACATCAAGAAGATCTTCGAGTTCAAAGAGAGACCTCGGAACCGGGC 264

QY 70 eAsnGlyLysValLeuGlnIlePheAsnLysArgThrGlnGluLysPheAlaLeuLysMe 90

Db 265 CTTTTCGAAGTGTTTAGCTGAAGAGAGCAAGCAACTGGCAAGCTCTTTGCTGTAAGTG 324

QY 90 tLeuGlnAspCysProLysAlaArgArgGluValGluLeuHis-----Tr 105

Db 325 TATCCCTAAGAAGCGCTGAAGGGCAAGGAAGCAGCATAGAGAATGAGATAGCCGTCCT 384

QY 105 pArgAlaSerGlnCysProHisIleValArgIleValaspValTyrGluAsnLeuTyrAl 125

Db 385 GAGAAAGATTAGCATGAAATATTTGTTGCCCTGGAAGACATTTATGAAAGC----- 436

QY 125 aGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGlyGluLeuPheSerAr 145

Db 437 ----CCAAATCACCTGTACTTGGTCATGCAGCTGGTGTCCGGTGGAGAGCTGTTTGACCG 492

QY 145 gIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMetLysSe 165

Db 493 GATAGTGGAGAGGGG-----TTTATACAGAGAGGATGCCAGCACTCTGTATCCGCCA 546

QY 165 rIleGlyGluAlaIleGlnTyrIleuHisSerIleAsnIleAlaHisArgAspValLysPr 185

Db 547 AGTCTTGGACGCCGTGTACTATCTCCACAGAATGGGCATCGTCCACAGAGACCTCAAGCC 606

QY 185 oGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLysLeuThrAsppheG1 205

Db 607 CGAAATCTCTTGTACTACAGTCAAGATGAGGAGTGCCAAAATAATATGATCAGTCTTGG 666

QY 205 yPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCysTyrThrProTyrTy 225

Db 667 ATTGTCAAAAATGGAGGGCAAAGGAGATGTGATGTCCACTGCCTGTGGAACCTCCAGGCTA 726

QY 225 rValAlaProGluValLeuGlyProGluLysTyrAspLysSerCysAspMetTirpSerLe 245

Db 727 TGTGCTCTCTGAAGTCCTCGCCACAGAAACCTTACAGCAAAAGCCGTTGACTGCTGGTCCAT 786

QY 245 uGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyrSerAsnHisGlyLe 265

Db 787 CGGAGTGATTGCCTACATCTTGCTCTGCGGCTACCCCTCCTTTTATGATGAAAAAT----- 841

QY 265 uAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyrGluPheProAsnPr 285

Db 842 -----GACTCCAAGCTCTTTGAGCAGATCCTCAAGGCGGAATATGAGTTTGACTCTCC 894

QY 285 oGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsnLeuLeuLysThrGl 305

Db 895 CTACTGGGATGACATCTCCGACTCTGCAAAAAGACTTTCATTCCGAACTGATGGAGAAGGA 954

QY 305 uProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrpIleMetGlnSerTh 325

Db 955 CCCCATAAAAAGATACACGTGTGAGCAGGCAGCTCGGCACCCCATGGATCGTGGTGACAC 1014

QY 325 rLysValProGlnThrProLeuHisThrSer-----ArgValLeuLysGlu---As 341

Db 1015 AGCCCTCAACAAAAAC--ATCCACGAGTCCGTGAGCCCGCCAGATCCGGAATAACTTTGC 1071

QY 341 pLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArgVa 361

Db 1072 CAAGAGCAAAATGG-----AGACAAGCATTTAATGCCACGCGCGCTGCTGAGA-- 1117

QY 361 lAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsn 376

Db 1118 -CATATGAGAAAAACTACACCTCGGCAGCAGCCTGGACAGTTCAAAT 1162

RESULT 9

US-10-446-175-5

; Sequence 5, Application US/10446175

; Patent No. 6806073

; GENERAL INFORMATION:

; APPLICANT: Donoho, Greg

; APPLICANT: Scoville, John

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Abuin, Alejandro

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6806073el Human Kinase Proteins and

; TITLE OF INVENTION: Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0103-USA

; CURRENT APPLICATION NUMBER: US/10/446,175

; CURRENT FILING DATE: 2003-05-27

; PRIOR APPLICATION NUMBER: US/09/733,388

; PRIOR FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: US 60/169,428
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1671
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-446-175-5

Alignment Scores:

Pred. No.: 1,21e-40 Length: 1671
Score: 536.00 Matches: 135
Percent Similarity: 53.0% Conservative: 75
Best Local Similarity: 34.1% Mismatches: 145
Query Match: 25.5% Indels: 41
DB: 3 Gaps: 14

US-10-469-221-2 (1-396) x US-10-446-175-5 (1-1671)

QY 2 GlnGlyGlnSerProProValPro---PheProAlaProAlaProProProGlnProPro 20
Db 37 CAGCCCGAGCGCCCGGCATCCCGCCGCTCTGCGCCCGCGCCGCGCCCGCGGCC 96
QY 21 ThrProAlaLeuProHisProProAlaGlnProPro-----Pro 33
Db 97 CTCCCAGCGCG-----CCCCCGCGCTCTCTCGCGCGGGAAGTTGCGCGCGAGCCC 150
QY 34 ProPro-ProGlnGlnPheProGlnPheHisValLysSerGlyLeuGlnLeuLysLysAs 53
Db 151 GAGCCGCTCGTCGGCCATGGCCCGGAGAACGGCGAGAGCAGCTCCTCTCGGAAAAAGCA 210
QY 53 nAlaIleIleAspTyrLysValThr-----SerGlnValLeuGlyLeuGlyI1 70
Db 211 AGCT-----GAAGACATCAAGAAGATCTTCGAGTTCAAAGAGAGACCCCTCGGAACCGGGC 264
QY 70 eAsnGlyLysValLeuGlnIlePheAsnLysArgThrGlnGluLysPheAlaLeuLysMe 90
Db 265 CTTTCCGAAGTGGTTTAGCTGAAGAGAGGCAACTGGCAAGCTCTTTGCTGTGAAGTG 324
QY 90 tLeuGlnAspCysProLysAlaArgArgGluValGluLeuHis-----Tr 105
Db 325 TATCCCTAAGAAGGCGCTGAAGGGCAAGGAAGCAGCATAGAGAAATGAGATAGCCGTCCT 384
QY 105 pArgAlaSerGlnCysProHisIleValArgIleValAspValTyrGluAsnLeuTyrAl 125
Db 385 GAGAAAGATTAAAGCATGAAATATTGTTGCCCTGGAAGACATTATGAAAGC-----436
QY 125 aGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGlyGluLeuPheSerAr 145
Db 437 -----CCAAATCCTGTACTTGGTCAATGCAGTGGTGTCCGGTGGAGAGCTGTTGACCG 492
QY 145 gIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMetLysSe 165
Db 493 GATAGTGGAGAGGGG-----TTTTATACAGAGAAGGATGCCAGCACTCTGATCCGCCA 546
QY 165 rIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHisArgAspValLysPr 185
Db 547 AGTCTTGACGCGGTGTACTATCTCCACAGATGGGCACTCGTCCACAGAGACCTCAAGCC 606
QY 185 oGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLysLeuThrAspPheG1 205
Db 607 CGAAATCTCTTGTTACTACAGTCAAGATGAGGAGTCCAAATAATGATCAGTACTTGG 666
QY 205 yPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCysTyrThrProTyrTy 225
Db 667 ATTGTCAAAAAATGGAGGGCAAAGGAGATGTGATGTCCACTGCCTGTGGAACTCCAGGCTA 726
QY 225 rValAlaProGluValLeuGlyProGluLysTyrAspLysSerCysAspMetTrpSerLe 245
Db 727 TGTGCTCCTGAAGTCTCGCCAGAAACCTTACAGCAAAAGCCGTTGACTGCTGTTCCAT 786
QY 245 uGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyrSerAsnHisGlyLe 265

Db 787 CGGAGTGATTGCCTACATCTTGCTCTGCGGTACCCCTCTCTTTTATGATGAAAAAT--- 841
QY 265 uAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyrGluPheProAsnPr 285
Db 842 -----GACTCCAAGCTCTTTAGCAGATCCTCAAGGCGGAATATGAGTTGACTCTCC 894
QY 285 oGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsnLeuLeuLysThrG1 305
Db 895 CTACTGGGATGACATCTCCGACTCTGCAAAAGACTTCATTCCGAACCTGATGGAGAAGGA 954
QY 305 uProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrpIleMetGlnSerTh 325
Db 955 CCCGAATAAAAGATACACGTGTGAGCAGGAGCTCGGCACCCCATGGATCGCTGGTGACAC 1014
QY 325 rLysValProGlnThrProLeuHisThrSer-----ArgValLeuLysGlu---As 341
Db 1015 AGCCCTCAACAAAAAC---ATCCACGAGTCCGTCAGCGCCAGATCCGGAAAAAATTTCG 1071
QY 341 pLysGluArgTrpGluAspValLysGluMetThrSerAlaLeuAlaThrMetArgVa 361
Db 1072 CAAGAGCAATGG-----AGACAAGCATTTAATGCCACGCCGCTCGTGAGA-- 1117
QY 361 lAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsn 376
Db 1118 -CATATGAGAAAACTACACCTCGGCAGCAGCCTGGACAGTTCAAAT 1162

RESULT 10

US-09-620-312D-526
; Sequence 526, Application US/09620312D
; Patent No. 659662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yuning
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 659662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 526
; LENGTH: 1733
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (215)..(1372)
US-09-620-312D-526

Alignment Scores:
Pred. No.: 2.72e-40 Length: 1733
Score: 532.50 Matches: 134
Percent Similarity: 53.4% Conservative: 73

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Best Local Similarity: 34.5% Mismatches: 138
Query Match: 25.3% Indels: 44
DB: 3 Gaps: 13

US-10-469-221-2 (1-396) x US-09-620-312D-526 (1-1733)

QY 14 AlaProProGlnProPro--ThrProAlaLeuProHisProProAlaGlnProPro 32
   ||||| |||:::||||| ||||| ||||| ||||| ||||| |||||
Db 102 GCGCGCAGCCCGAGCCGCGGCATCCCCCGCCCTCTGCGCCCGC-GCCGCGCCCG 160
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 33 ProProProGlnPhePro----- 40
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 161 GCGCCCCCTCCCCAGCGCGCCCCCGCGCTCCTCCGCGCGCGCTCGTCGGCCATGGCC 220
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 41 GlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleIleAspAspTyrLys 60
   :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 221 CGGAGAACGGCAGACAGCTCTCTTGAAAAAGCAAGCT-----GAAGACATCAAG 274
   :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
QY 61 ValThr-----SerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIle 77
   :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 275 AAGATCTTCGAGTTCAAAGAGACCCTCGGAACCGGGGCTTTCCGAAGTGGTTTAGCT 334
   :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
QY 78 PheAsnLysArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAla 97
   ||||| ||||| :::: :::: :::: :::: :::: :::: ::::
Db 335 GAAGAGAAGGCAACTGGCAAGCTCTTTGCTGTGAAGTGTATCCCTAAGAAGCGCTGAAG 394
   ||||| ||||| :::: :::: :::: :::: :::: :::: ::::
QY 98 ArgArgGluValGluLeuHis-----TrpArgAlaSerGlnCysProHis 112
   :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 395 GGCAAGGAAAGCAGCATAGAGAATGAGATAGCCGCTCTGAGAAAGATTAAGCATGAAAAAT 454
   :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
QY 113 IleValArgIleValAspValTyrGluAsnLeuTyrAlaGlyArgLysCysLeuLeuIle 132
   ||||| :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 455 ATTGTTGCCCTGGAAACATTTATGAAAGC-----CCAAATCACCTGTACTGTG 502
   ||||| :::: :::: :::: :::: :::: :::: :::: :::: ::::
QY 133 ValMetGluCysLeuAspGlyGlyGluLeuPheSerArgIleGlnAspArgGlyAspGln 152
   ||||| :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 503 GTCATGCAGCTGGTGTCCGGTGGAGAGCTGTTTGACCGGATAGTGGAGAAGGG----- 556
   ||||| :::: :::: :::: :::: :::: :::: :::: :::: ::::
QY 153 AlaPheThrGluArgGluAlaSerGluIleMetLysSerIleGlyGluAlaIleGlnTyr 172
   :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 557 TTTTATACAGAGAAGGATGCCAGCACTCTGATCCGCCAAGTCTTGGACGCCGTGACTAT 616
   ||||| :::: :::: :::: :::: :::: :::: :::: :::: ::::
QY 173 LeuHisSerIleAsnIleAlaHisArgAspValLysProGluAsnLeuLeuTyrThrSer 192
   ||||| :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 617 CTCCACAGAATGGGCATCGTCCACAGAGACCTCAAGCCCGAAAAATCTCTTGTTACTACAGT 676
   ||||| :::: :::: :::: :::: :::: :::: :::: :::: ::::
QY 193 LysArgProAsnAlaIleLeuLysLeuThrAspPheGlyPheAlaLysGluThrThrSer 212
   :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 677 CAAGATGAGGAGTCCAAAAATAATGATCAGTGACTTTGGATTGTCAAAAAATGGAGGCAAA 736
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 213 HisAsnSerLeuThrThrProCysTyrThrProTyrTyrValAlaProGluValLeuGly 232
   :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 737 GGAGATGTGATGTCCATGCCTGTGGAACTCCAGGCTATGTGCTCTCTGAAGTCTCTGCGC 796
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 233 ProGluLysTyrAspLysSerCysAspMetTrpSerLeuGlyValIleMetTyrIleLeu 252
   :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 797 CAGAAACCTTACAGCAAAAGCCGTTGACTGCTGGTCCATCGGAGTGATTGCCTACATCTTG 856
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 253 LeuCysGlyTyrProPheTyrSerAsnHisGlyLeuAlaIleSerProGlyMetLys 272
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 857 CTCTGGGCTACCTCTCTTTTATGATGAAAAAT-----GACTCCAAGCTCTTT 904
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 273 ThrArgIleArgMetGlyGlnTyrGluPheProAsnProGluTrpSerGluValSerGlu 292
   :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 905 GAGCAGATCCTCAAGGCGGAATATGAGTTTGACTCTCCCTACTGGGATGACATCTCCGAC 964
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 293 GluValLysMetLeuIleArgAsnLeuLeuLysThrGluProThrGlnArgMetThrIle 312
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 965 TCTGCAAAAGACTTCATTTCGGAACCTGATGGAGAAGGACCCGAATAAAAGATACACGTGT 1024
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 313 ThrGluPheMetAsnHisProTrpIleMetGlnSerThrLysValProGlnThrProLeu 332
   :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
Db 1025 GAGCAGGCAGCTCGGCACCATGGATCGTGGTGCACAGCCCTCAACAAAAAC---ATC 1081
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

[illegible]

QY 122 AsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGlyGlu 141
Db 510 AGC-----CCAAATCACCTCTACCTGGTCATGCAACTTGTGTCTGGTGAGAA 557
QY 142 LeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSerGlu 161
Db 558 CTCTTCGATCGGATAGTGAGAGGG-----TTTACACAGAGAAAGATGCCAGCACT 611
QY 162 IleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHisArg 181
Db 612 CTCATCCGCCAGGTCCTGGATGCGGTATACTATCTCCACAGAATGGGCATTTGCCACAGG 671
QY 182 AspValLysProGluAsnLeuTyrThrSerLysArgProAsnAlaIleLeuLysLeu 201
Db 672 GACCTCAAGCCGGAGATCTCTTATACTACAGTCAAGCAGGAGTCCAAAATAATGATC 731
QY 202 ThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCysTyr 221
Db 732 AGTGACTTTGGCTTGTGAAAATGGAGGGCAAAGGAGATGTGATGTCCACGCCCTGCGGG 791
QY 222 ThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCysAsp 241
Db 792 ACCCCAGGCTATGTTGCTCCGGAAGTTCTCGCCAGAAAACCGTACAGCAAAGCTGTGGAC 851
QY 242 MetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyrSer 261
Db 852 TGCTGGTCCATCGGGGTGATCGCCTATATCTTGCTGTGTGTTACCTCCTTTTATGAT 911
QY 262 AsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyrGlu 281
Db 912 GAAAAT-----GACTCGAAGCTGTTTGAACAGATCCTCAAGGCAGATATGAG 959
QY 282 PheProAsnProGluTrpSerGluValSerGluValLysMetLeuIleArgAsnLeu 301
Db 960 TTTGATTCCCCCTACTGGGATGACATCTCCGACTCTGCCAAAGACTTTCATTCCGAATCTG 1019
QY 302 LeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrpIle 321
Db 1020 ATGGAGAAAGACCCCAATAAAGATACACTTGTGAGCAGGCAGCTCGACACCCATGGATT 1079
QY 322 MetGlnSerThrLysValProGlnThrProLeuHisThrSer-----ArgValLeu 338
Db 1080 GCTGGTGACACAGCCCTTAGCAAAAAC---ATTACAGAAATCTGTGAGTCCACAGATCCGG 1136
QY 339 LysGlu---AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAla 357
Db 1137 AAGAATTTTGCAAGAGACAAATGG-----AGACAAGCGTTTAAAGCCACGGCA 1184
QY 358 ThrMetArgValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsn 376
Db 1185 GTCGTGAGA---CATATGCGGAGGCTCCAGCTTGGCAGCAGCCTGGACAGTTCAAAAT 1238

RESULT 12
US-10-355-975A-3
; Sequence 3, Application US/10355975A
; Patent No. 6759223
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
; FILE REFERENCE: 2923-B
; CURRENT APPLICATION NUMBER: US/10/355,975A
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1694
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-355-975A-3

Alignment Scores:
Pred. No.: 5,03e-40 Length: 1694
Score: 529.50 Matches: 136
Percent Similarity: 51.9% Conservative: 71
Best Local Similarity: 34.1% Mismatches: 138
Query Match: 25.1% Indels: 56
DB: 3 Gaps: 13
US-10-469-221-2 (1-396) x US-10-355-975A-3 (1-1694)

QY 9 PropheProAlaProAlaProProGlnProProThrProAlaLeuProHisProPro 28
Db 113 CCGGAGCCTCCCTCGCTCCGCATCCTCCCGCTCCGCATCCCGGCGCCGGGCATCCCCCG 172
QY 29 AlaGlnProProProProGlnGlnPheProGlnPheHisValLysSerGlyLeu 48
Db 173 ---GAGCCCGCGCGCG-CTTCCGGCGCCCTTCCCAGCG-CAACCCCTCGGCCCCCTA 227
QY 49 Gln-----Gln----- 49
Db 228 CAGCATTAGTCTGCCATGGCCCCGGAGAACGGCGAGAGCAGCTCCTCTCGAAAAAGCAA 287
QY 50 -----IleLysLysAsnAlaIleIleAspAspTyrLysValThrSerGlnValLeu 66
Db 288 GCAGAAAGACATTAAGAAG-----ATCTTCGAGTTCAAGGAGACC-----CTC 329
QY 67 GlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLysArgThrGlnGluLysPhe 86
Db 330 GGAACTGGGGCTTTTCTGAAGTTGTTTAGCCGAGGAGAAAGCTACTGGGAAGCTCTTC 389
QY 87 AlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGluValGluLeuHis----- 104
Db 390 GCAGTGAAGTGCATCCCGAAGAGGCGCTGAAGGGCAAGGAGAGCAGCATCGAGAACGAG 449
QY 105 -----TrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyrGlu 121
Db 450 ATTGCCGTGCTTAGAAAGATTAAAGCATGAAACATTTGTCCTTGGAGATATTTATGAA 509
QY 122 AsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGlyGlu 141
Db 510 AGC-----CCAAATCACCTTACCTGGTGCATGCAACTTGTGTCTGGTGAGAA 557
QY 142 LeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSerGlu 161
Db 558 CTCTTCGATCGATAGTGGAGAGGG-----TTTACACAGAGAAAGATGCCAGCACT 611
QY 162 IleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHisArg 181
Db 612 CTCATCCGCCAGGCTCTGGATGCGGTATCTTATACTACAGTCAAGCAGGAGTCCAAAATAATGATC 731
QY 182 AspValLysProGluAsnLeuTyrThrSerLysArgProAsnAlaIleLeuLysLeu 201
Db 672 GACCTCAAGCCGGAGAAATCTCTTATACTACAGTCAAGCAGGAGTCCAAAATAATGATC 731
QY 202 ThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCysTyr 221
Db 732 AGTGACTTTGGCTTGTGAAAATGGAGGGCAAAGGAGATGTGATGTCCACGCCCTGCGGG 791
QY 222 ThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCysAsp 241
Db 792 ACCCCAGGCTATGTTGCTCCGGAAGTTCTGCCCCAGAAACCGTACAGCAAAGCTGTGGAC 851
QY 242 MetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyrSer 261
Db 852 TGCTGGTCCATCGGGGTGATCGCCTATATCTTGCTGTGTGTTACCTCCTTTTATGAT 911
QY 262 AsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyrGlu 281
Db 912 GAAAAT-----GACTCGAAGCTGTTTGAACAGATCCTCAAGGCAGAAATATGAG 959
QY 282 PheProAsnProGluTrpSerGluValSerGluValLysMetLeuIleArgAsnLeu 301

Db 960 TTTGATTCCCCCTACTGGGATGACATCTCCGACTCTGCCAAAGACTTCATTTCGGAATCTG 1019

QY 302 LeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrpIle 321
::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::

Db 1020 ATGGAGAAAGACCCAAATAAAGATACACTTGTGAGCAGGCAGCTCGACACCCATGGATT 1079

QY 322 MetGlnSerThrLysValProGlnThrProGlnThrProLeuHisThrSer-----ArgValLeu 338
||| :::: :::: :::: :::: :::: ||| :::: :::: :::: :::: ::::

Db 1080 GCTGGTGACACAGCCCTTAGCAAAAAC---ATTCACGAATCTGTCAAGTCCCGGATCCGG 1136

QY 339 LysGlu---AspLysGluArgTrpGluAspValLysGluMetThrSerAlaLeuAla 357
||| ||| :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::

Db 1137 AAGAATTTTGCAAGAGCAAAATGG-----AGACAAGCGTTTAAAGCCACGGCA 1184

QY 358 ThrMetArgValaspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsn 376
::: ||| :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::

Db 1185 GTCGTGAGA---CATATCGGAGGCTCCAGCTTGGCAGCAGCCTGGACAGTTCAAAT 1238

RESULT 13

US-09-980-464-3

; Sequence 3, Application US/09980464

; Patent No. 7001752

; GENERAL INFORMATION:

; APPLICANT: Immunex Corporation

; APPLICANT: Bird, Timothy A.

; APPLICANT: Virca, G. Duke

; APPLICANT: Martin, Unja

; APPLICANT: Anderson, Dirk M.

; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES

; FILE REFERENCE: 2923-US

; CURRENT APPLICATION NUMBER: US/09/980,464

; CURRENT FILING DATE: 2001-11-27

; NUMBER OF SEQ ID NOS: 36

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 1694

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-980-464-3

Alignment Scores:

Pred. No.:	5.03e-40	Length:	1694
Score:	529.50	Matches:	136
Percent Similarity:	51.9%	Conservative:	71
Best Local Similarity:	34.1%	Mismatches:	138
Query Match:	25.1%	Indels:	56
DB:	5	Gaps:	13

US-10-469-221-2 (1-396) x US-09-980-464-3 (1-1694)

QY 9 ProPheProAlaProAlaProProGlnProProThrProAlaLeuProHisProPro 28
||| ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

Db 113 CCCGAGCCTCCCTGGCTCCGCATCCTCCCGCTCCGCATCCCGGCGCGCGGCATCCCCCG 172

QY 29 AlaGlnProProProProGlnGlnPheProGlnPheHisValLysSerGlyLeu 48
::: ||| ||| |||| |||| |||| |||| |||| |||| |||| ::::

Db 173 ---GAGCCCGCGCGCG-CCTCCGGCGCCCTTCCCCAGCG-CAACCCCTCGCGCCCTA 227

QY 49 Gln----- 49

Db 228 CAGCATTAGTCTGCCATGGCCCGGAGAACGGCGAGAGCAGCTCCTCTGGAAAAAGCAA 287

QY 50 -----IleLysLysAsnAlaIleIleaspAspTyrLysValThrSerGlnValLeu 66
||| |||| |||| |||| :::: :::: ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 288 GCAGAAGACATTAGAAG-----ATCTTCGAGTTCAGGAGACC-----CTC 329

QY 67 GlyLeuGlyIleAsnGlyLysValLeuGlnIlePheAsnLysArgThrGlnGluLysPhe 86
||| ||| :::: :::: :::: :::: :::: ||| ||| ||| ||| ::::

Db 330 GGAAGTGGGCGCTTTTCTGAAGTTGTTTTAGCCGAGGAGAAAGCTACTGGGAAGCTCTTC 389

QY 87 AlaLeuLysMetLeuGlnAspCysProLysAlaArgArgGluValGluLeuHis----- 104
||| :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::

Db 390 GCAGTGAAGTGCATCCCGAAGAAGCGGCTGAAGGCAAGGAGAGCAGCATCGAGAACGAG 449

QY 105 -----TrpArgAlaSerGlnCysProHisIleValArgIleValAspValTyrGlu 121
||| :::: :::: |||| |||| :::: |||| :::: |||| :::: |||| :::: ||||

Db 450 ATTGCCGTGCTTAGAAAAGATTAAAGCATGAAAACATTGTTGCCTTGGAGATATTTATGAA 509

QY 122 AsnLeuTyrAlaGlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGlyGlu 141
::: ||| :::: |||| :::: |||| :::: |||| :::: |||| :::: |||| :::: ||||

Db 510 AGC-----CCAAATCACCTCTACCTGGTCACTGCAACTGTGTCTGGTGGAGAA 557

QY 142 LeuPheSerArgIleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSerGlu 161
|||| ||| |||| :::: :::: :::: :::: :::: |||| :::: |||| :::: ||||

Db 558 CTCCTTCGATCGGATAGTGGAGAGGGG-----TTTTACACAGAGAAAGATGCCAGCACT 611

QY 162 IleMetLysSerIleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHisArg 181
::: :::: :::: :::: |||| :::: |||| :::: |||| :::: |||| :::: ||||

Db 612 CTCATCCGCCAGGTCCTGGATGCCGTATACTATCTCCACAGAAATGGGCATTGTCCACAGG 671

QY 182 AspValLysProGluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLysLeu 201
||| :::: |||| |||| |||| |||| |||| |||| :::: :::: :::: :::: ::::

Db 672 GACCTCAAGCCGGAGAATCTCTTATACTACAGTCAAGACGAGGAGTCCAAAATAATGATC 731

QY 202 ThrAspPheGlyPheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCysTyr 221
::: |||| |||| :::: ||| :::: :::: :::: :::: |||| :::: ||||

Db 732 AGTGACTTTGGCTTGTGCGAAAATGGAGGGGCAAAGAGAGATGTGATGTCCACGGCCTGCGGG 791

QY 222 ThrProTyrTyrValAlaProGluValLeuGlyProGluLysTyrAspLysSerCysAsp 241
|||| ||| |||| |||| |||| |||| |||| :::: |||| :::: |||| :::: ||||

Db 792 ACCCCAGGCTATGTTGCTCCGGAAGTTCTCGCCCAAGAACCGTAGACAGCAAAAGCTGTGGAC 851

QY 242 MetTrpSerLeuGlyValIleMetTyrIleLeuLeuCysGlyTyrProPheTyrSer 261
|||| :::: |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||

Db 852 TGCTGGTCCATCGGGGTGATCGCCTATATCTTGCTCTGTGTTACCTCCTTTTATGAT 911

QY 262 AsnHisGlyLeuAlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyrGlu 281
::: :::: :::: |||| :::: |||| :::: |||| :::: |||| :::: ||||

Db 912 GAAAAT-----GACTCGAAGCTGTTTGAACAGATCCTCAAGGCAGAATATGAG 959

QY 282 PheProAsnProGluTrpSerGluValSerGluGluValLysMetLeuIleArgAsnLeu 301
||| :::: |||| ||| :::: |||| :::: |||| :::: |||| :::: |||| :::: ||||

Db 960 TTTGATTCCCCCTACTGGGATGACATCTCCGACTCTGCCAAAGACTTCATTTCGGAATCTG 1019

QY 302 LeuLysThrGluProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrpIle 321
::: :::: :::: |||| |||| :::: :::: |||| :::: |||| :::: |||| :::: ||||

Db 1020 ATGGAGAAAGACCCAAATAAAAGATACACTTGTGAGCAGGCAGCTCGACACCCATGGATT 1079

QY 322 MetGlnSerThrLysValProGlnThrProLeuHisThrSer-----ArgValLeu 338
||| :::: ||| :::: :::: |||| :::: |||| :::: |||| :::: ||||

Db 1080 GCTGGTGACACAGCCCTTAGCAAAAAC---ATTACGAATCTGTCAAGTCCCGATCCGG 1136

QY 339 LysGlu---AspLysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAla 357
||| ||| :::: |||| :::: |||| :::: |||| :::: |||| :::: ||||

Db 1137 AAGAATTTTGCAAGAGCAAAATGG-----AGACAAGCGTTTAAAGCCACGGCA 1184

QY 358 ThrMetArgValAspTyrGluGlnIleLysIleLysLysIleGluAspAlaSerAsn 376
::: |||| :::: :::: :::: :::: :::: |||| :::: |||| :::: ||||

Db 1185 GTCGTGAGA---CATATCGGAGGCTCCAGCTTGGCAGCAGCCTGGACAGTTCAAAT 1238

RESULT 14

US-09-949-016-1590

; Sequence 1590, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1590
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1590

Alignment Scores:
Pred. No.:      1.63e-39      Length:      1442
Score:          523.00        Matches:      125
Percent Similarity: 54.3%      Conservative: 70
Best Local Similarity: 34.8%      Mismatches:  126
Query Match:    24.8%         Indels:       38
DB:              3           Gaps:        11

US-10-469-221-2 (1-396) x US-09-949-016-1590 (1-1442)

QY 18 GlnProProThrProAlaLeuProHisProProAlaGlnProProProProGln 37
   |||||||
   ::::
69 CAACCACCGCGGCTCCAGCCAGCCCGCGGGGAGCCCTGGCTGTGGTGGGGG 128
   |||
38 GlnPheProGlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleAsp 57
   |||
129 CAGTGGCCATGTGGGGGCAGTGAAGGCCCCAGGTGAAGCAGCGCGGAGACATTAGA 188
   |||
58 AspTyrLysValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIle 77
   |||
189 GACATCTACGACTTCCGAGATGTTCTGGGCACGGGGGCCCTTCTCGGAGGTGATCCTGGCA 248
   |||
78 PheAsnLysArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAla 97
   ::::
249 GAAGATAAGAGGACGAGAGCTGGTGGCCATCAAAATGCATT-----GCC 293
   |||
98 ArgArgGluValGlu-----LeuHisTrp 105
   ::
294 AAGGAGGCCCTGGAGGGCAAGGAAGGCAGCATGGAGAATGAGATTGCTGCTGCAC--- 350
   |||
106 ArgAlaSerGlnCysProHisIleValArgIleValAspValTyrGluAsnLeuTyrAla 125
   ::
351 ---AAGATCAAGCACCCCAACATTGTAGCCCTGGATGACATCTATGAGAGT-----GGG 401
   |||
126 GlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGlyGluLeuPheSerArg 145
   |||
402 GGCCAC-----CTCTACCTCATCATGCAGTGTGTGGTGGGAGGCTTTTGACCGT 455
   |||
146 IleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMetLysSer 165
   |||
456 ATTGTGAAAAAGGC-----TTCTACACGGAGCGGACGCCAGCCGCTCATCTTCAG 509
   |||
166 IleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHisArgAspValLysPro 185
   ::
510 GTGCTGGATGCTGTGAATACCTGCATGACCTGGGCATTGTACACCGGGATCTCAAGCCA 569
   |||
186 GluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLysLeuThrAspPheGly 205
   |||
570 GAGAATCTGCTGTACTACAGCCTGGATGAAGACTCCAAATCATGATCTCCGACTTTGGC 629
   |||
206 PheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCysTyrThrProTyrTyr 225
   ::
630 CTCTCCAAGATGGAGGACCCGGGCAGTGTGCTCTCCACCGCTGTGGAACCTCCGGGATAC 689
   |||
226 ValAlaProGluValLeuGlyProGluLysTyrAspLysSerCysAspMetTrpSerLeu 245
   |||
690 GTGGCCCTGAATCTCTGGCCAGAACCCCTACAGCAAGGCTGTGGAATGCTGTGTCATA 749
   |||
246 GlyValIleMetTyrIleLeuLeuCysGlyTyrProProPheTyrSerAsnHisGlyLeu 265
   |||
750 GGTGTATCGCTACATCTTGCTCTCGGTTACCTCCCTCTCTATATGACGAGAATGATGCC 809
   |||
266 AlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyrGluPheProAsnPro 285
   ::
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Db 810 AAACCTCTTT-----GAACAGATTTTGAAGGCCGAGTACGAGTTTGACTCTCCT 857
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QY 306 ProThrGlnArgMetThrIleThrGluPheMetAsnHisProTrpIleMetGlnSerThr 325
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Db 918 CCAGAGAAAAGATTACCTGTGAGCAGGCCCTTGACGCCCATGGATTGCAGGAGATACA 977
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QY 326 LysValProGlnThrProLeuHis-----ThrSerArgValLeuLysGluAsp----- 341
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Db 978 GCTCTAGATAAGAAT---ATCCACCAGTCCGTGGTGAGTGAGCATCAAGAAGAACTTTGCC 1034
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QY 342 LysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360
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RESULT 15
US-09-949-016-1591
; Sequence 1591, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1591
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1591
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Score:          523.00        Matches:      125
Percent Similarity: 54.3%      Conservative: 70
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QY 38 GlnPheProGlnPheHisValLysSerGlyLeuGlnIleLysLysAsnAlaIleAsp 57
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Db 129 CAGTGGGCCATGTCTGGGGGCAGTGAAGGCCCCAGGTGAAGCAGCGCGGAGACATTAGA 188
   |||
QY 58 AspTyrLysValThrSerGlnValLeuGlyLeuGlyIleAsnGlyLysValLeuGlnIle 77
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Db 189 GACATCTACGACTTCCGAGATGTTCTGGGCACGGGGGCCCTTCTCGGAGGTGATCCTGGCA 248
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QY 78 PheAsnLysArgThrGlnGluLysPheAlaLeuLysMetLeuGlnAspCysProLysAla 97
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Db 249 GAAGATAAGAGGACGAGAGCTGGTGGCCATCAAAATGCATT-----GCC 293
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QY 98 ArgArgGluValGlu-----LeuHisTrp 105
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294 AAGGAGGCCCTGGAGGGCAAGGAAGGCAGCATGGAGAATGAGATTGCTGCTGCAC--- 350
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QY      126 GlyArgLysCysLeuLeuIleValMetGluCysLeuAspGlyGlyGluLeuPheSerArg 145
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QY      146 IleGlnAspArgGlyAspGlnAlaPheThrGluArgGluAlaSerGluIleMetLysSer 165
Db      456 ATTGTGGAATAAGGC-----TTCTACCGAGCGGGACGCCCGCCTCATCTTCCAG 509

QY      166 IleGlyGluAlaIleGlnTyrLeuHisSerIleAsnIleAlaHisArgAspValLysPro 185
Db      510 GTGCTGGATGCTGTGAATAACCTGCATGACCTGGGCATTGTACACCGGGATCTCAAGCCA 569

QY      186 GluAsnLeuLeuTyrThrSerLysArgProAsnAlaIleLeuLysLeuThrAspPheGly 205
Db      570 GAGAAATCTGCTGTACTACAGCCTGGATGAAGACTCCAAAAATCATGATCTCCGACTTTGGC 629

QY      206 PheAlaLysGluThrThrSerHisAsnSerLeuThrThrProCysTyrThrProTyrTyr 225
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QY      226 ValAlaProGluValLeuGlyProGluLysTyrAspLysSerCysAspMetTrpSerLeu 245
Db      690 GTGGCCCTGAAGTCTCTGGCCAGAGCCCTACAGCAAGGCTGTGGATTGCTGGTCCATA 749

QY      246 GlyValIleMetTyrIleLeuLeuCysGlyTyrProPheTyrSerAsnHisGlyLeu 265
Db      750 GGTGTCTATCGCCTACATCTTGTCTCGGGTTACCCCTCCCTTCTATGACGAGAATGATGCC 809

QY      266 AlaIleSerProGlyMetLysThrArgIleArgMetGlyGlnTyrGluPheProAsnPro 285
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QY      286 GluTrpSerGluValSerGluGluValLysMetLeuIleArgAsnLeuLeuLysThrGlu 305
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Db      918 CCAGAGAAAAGATTCACTGTGAGCAGGCTTGCAGCACCCCATGGATTGCAGGAGATACA 977

QY      326 LysValProGlnThrProLeuHis-----ThrSerArgValLeuLysGluAsp----- 341
Db      978 GCTCTAGATAAGAAT---ATCCACCAGTCGGTGAAGTGAGCAGATCAAGAAGAACTTTGCC 1034

QY      342 LysGluArgTrpGluAspValLysGluGluMetThrSerAlaLeuAlaThrMetArg 360
Db      1035 AAGAGCAAGTGG-----AAGCAAGCCTTCAATGCCACGGCTGTGGTGGCGG 1079
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GenCore version 5.1.9
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Run on: June 19, 2006, 16:04:24 ; Search time 261 Seconds
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 2807332

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1181.4	99.2	1336	3 US-09-023-655-1397	Sequence 1397, Ap
2	1048.4	88.0	2258	3 US-09-016-434-1415	Sequence 1415, Ap
3	555.8	46.7	2481	3 US-09-016-434-1088	Sequence 1088, Ap
4	555.8	46.7	2482	3 US-09-949-016-5682	Sequence 5682, Ap
5	555.8	46.7	2509	3 US-09-949-016-660	Sequence 660, App
6	528	44.3	1333	3 US-09-142-551A-1	Sequence 1, Appli
7	142.2	11.9	438	4 US-09-880-107-810	Sequence 810, App
8	126.4	10.6	1442	3 US-09-949-016-1590	Sequence 1590, Ap
9	126.4	10.6	1442	3 US-09-949-016-1591	Sequence 1591, Ap
10	122.6	10.3	1694	3 US-09-579-664B-3	Sequence 3, Appli
11	122.6	10.3	1694	3 US-10-355-975A-3	Sequence 3, Appli
12	122.6	10.3	1694	5 US-09-980-464-3	Sequence 3, Appli
13	122.2	10.3	1480	3 US-09-016-434-1454	Sequence 1454, Ap
14	120.4	10.1	1282	2 US-08-878-989-12	Sequence 12, Appl
15	120.4	10.1	1282	3 US-09-272-796-12	Sequence 12, Appl
16	120.4	10.1	1282	3 US-09-016-434-953	Sequence 953, App
17	120	10.1	1584	3 US-09-799-451-205	Sequence 205, App
18	117.8	9.9	1458	3 US-09-230-896C-5	Sequence 5, Appli
19	111	9.3	1733	3 US-09-620-312D-526	Sequence 526, App
20	109.8	9.2	1074	3 US-09-733-388-3	Sequence 3, Appli
21	109.8	9.2	1074	3 US-10-446-175-3	Sequence 3, Appli
22	109.8	9.2	1158	3 US-09-733-388-1	Sequence 1, Appli
23	109.8	9.2	1158	3 US-10-446-175-1	Sequence 1, Appli

24	109.8	9.2	1671	3 US-09-733-388-5	Sequence 5, Appli
25	109.8	9.2	1671	3 US-10-446-175-5	Sequence 5, Appli
26	104.8	8.8	3471	2 US-08-715-568A-2	Sequence 2, Appli
27	100.8	8.5	2447	3 US-09-960-643-1	Sequence 1, Appli
28	100	8.4	3061	4 US-09-880-107-2146	Sequence 2146, Ap
29	94.6	7.9	1847	3 US-09-949-016-5449	Sequence 5449, Ap
30	93	7.8	5926	3 US-09-917-254-41	Sequence 41, Appl
31	93	7.8	5926	4 US-09-880-107-3371	Sequence 3371, Ap
32	92.4	7.8	1158	3 US-10-843-136-1	Sequence 1, Appli
33	92.4	7.8	1158	3 US-10-116-332-1	Sequence 1, Appli
34	92.4	7.8	1167	3 US-09-940-921B-6	Sequence 6, Appli
35	92.4	7.8	1197	3 US-09-940-921B-8	Sequence 8, Appli
36	92.4	7.8	1744	3 US-09-940-921B-10	Sequence 10, Appl
37	85.4	7.2	2218	3 US-09-820-790B-1	Sequence 1, Appli
38	84.2	7.1	1429	2 US-09-159-385-4	Sequence 4, Appli
39	84.2	7.1	1429	3 US-09-186-277-4	Sequence 4, Appli
40	84.2	7.1	3228	3 US-09-579-664B-5	Sequence 5, Appli
41	84.2	7.1	3228	3 US-10-355-975A-5	Sequence 5, Appli
42	84.2	7.1	3228	5 US-09-980-464-5	Sequence 5, Appli
43	84.2	7.1	3503	3 US-09-823-038A-58	Sequence 58, Appl
44	83.6	7.0	1349	2 US-07-951-715A-20	Sequence 20, Appl
45	83.6	7.0	1349	2 US-08-459-448A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1

US-09-023-655-1397

; Sequence 1397, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; TITLE OF INVENTION: EXPRESSION

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/023,655

; FILING DATE: HERewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0001 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 1397:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1336 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GENBANK

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; CLONE: 9407074
US-09-023-655-1397

Query Match
Best Local Similarity 99.2%; Score 1181.4; DB 3; Length 1336;
Matches 1185; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCCCGCGCCCCCGCGCAGCCCCC 60
Db 1 TCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCCCGCGCCCCCGCGCAGCCCCC 60

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Db 61 ACCCCTGCCCTGCCGACCCCCCGGCGAGCCGCGCGCGCGCCCCCGCAGCAGTTCCCG 120

QY 121 CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCCATATCGATGACTACAAG 180
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QY 181 GTCACCAGCCAGTCCTGGGGCTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG 240
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QY 241 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCAGGCCCGCAGGGAG 300
Db 241 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCAGGCCCGCAGGGAG 300

QY 301 GTGGAGCTGCACCTGGCGGGCCTCCCAGTGGCCGCACATCGTACGGATCGTGGATGTGTAC 360
Db 301 GTGGAGCTGCACCTGGCGGGCCTCCCAGTGGCCGCACATCGTACGGATCGTGGATGTGTAC 360

QY 361 GAGAACTGTACGCGAGGGAGGAAGTGCCCTGCTGATTGTCATGGAATGTTTGGACGGTGA 420
Db 361 GAGAACTGTACGCGAGGGAGGAAGTGCCCTGCTGATTGTCATGGAATGTTTGGACGGTGA 420

QY 421 GAACTCTTTAGCCGAATCCAGGATCGAGGACCAAGGCATTCACAGAAAGAGAGCATCC 480
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QY 481 GAAATCATGAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 540
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QY 781 TCCAAACACGGCCTTGCCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCCAGTAT 840
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QY 841 GAATTTCCCAACCCAGAAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
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QY 901 CTGCTGAAAACAGAGCCCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 960
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QY 1081 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAAACCCTCTGTGCTG 1140
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QY 1141 AAGAGCGGAAGAAAGCTCGGGCCTGGAGGCTGCGGCTCTGGCCCACTGA 1191
Db 1141 AAGAGCGGAAGAAAGCTCGGGCCTGGAGGCTGCGGCTCTGGCCCACTGA 1191

RESULT 2
US-09-016-434-1415
; Sequence 1415, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1415:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2258 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9530089
US-09-016-434-1415

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Best Local Similarity 99.9%; Score 1048.4; DB 3; Length 2258;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 391 TCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCCCGCGCCCCCGCAGCCCCC 450

QY 61 ACCCCTGCCCTGCCGACCCCCCGGCGAGCCGCGCGCGCCCCCGCAGCAGTTCCCG 120
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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 660
; LENGTH: 2509
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-660

Query Match 46.7%; Score 555.8; DB 3; Length 2509;
Best Local Similarity 72.4%; Pred. No. 5.8e-120;
Matches 735; Conservative 0; Mismatches 277; Indels 3; Gaps 1;

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210 GCGGGAGCCCAAGAGTACGCAGTACCGACGACTACCAGTTGTCCAAGCAGGTGCTGG 269
QY 200 GGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAGAGGACCCAGGAGAAATTCG 259
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270 GCCTGGGTGTGAACGGCAAGTGTCTGGAGTGTCTTCCATCGGCGCACTGGACAGAAGTGTG 329
QY 260 CCCTCAAAATGCTTCAGGACTGCCCAAGCCCGCAGGGAGGTGGAGCTGCACTGGCGGG 319
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330 CCCTGAAGTCTCTGTATGACAGCCCAAGCCCGCAGGAGGTAGACCATCACTGGCAGG 389
QY 320 CCTCCAGTGCCTGCATCGTACGGATCGTGGATGTGTACGAGAAATCTGTACGCAGGGA 379
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390 CTTCTGGCGGCCCCCATATTGTCTGCATCCTGGATGTGTATGAGAACATGCACCATGGCA 449
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450 AGCGTGTCTCTCATCATGGAATGCATGGAGGTGGTGAAGTGTGTTACGAGGATTC 509
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570 GCACTGCCATCCAGTTCTGCACAGCCATAACATTTGCCACCGAGATGTCAAGCCTGAAA 629
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630 ACCTACTCTACACATCTAAGGAGAGAAAGACGCGAGTGTCTAAGCTCACCGATTTTGGCTTTG 689
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QY 680 CTCAGAAAGTCTGGTCCAGAGAAGTATGACAAAGTCTCTGTGACATGTGTGCTCCCTGGGTG 739
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747 CCCCTGAGGTCTGGTCCAGAGAAGTATGACAAAGTCAATGTGACATGTGTGCTCCCTGGGTG 806
QY 740 TCATCATGTACATCTCTGTTGGGTATCCCCCTTCTACTCCAACACCGGCTTTGCCA 799
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
807 TCATCATGTACATCTCTTGTGGCTTCCCACTTCTACTCCAACACCGGCTTGGCCA 866
QY 800 TCTCTCCGGGCATGAAGACTCGCATCCGAATGGCCAGTATGAATTTCCCAACCCAGAAT 859
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
867 TCTCCCCGGGATGAAGAGGAGGATTCGCTGGCCAGTACGGCTTCCCAATCTCTGAGT 926
QY 860 GGTCAAGATATCAGAGGAAGTGAAGATGTCTCAATTCGGAATCTGCTGAAACAGAGCCCA 919
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 927 GGTCAGAAAGTCTCTGAGGATGCCAAGCAGCTGATCCGCCTCCTGTTGAAGACAGACCCCA 986
QY 920 CCCAGAGAATGACCATCACCGAGTTTATGAACCACCCCTTGGATCATGCAATCAACAAAGG 979
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
987 CAGAGAGGCTGACCATCACTCAGTTTCATGAACACACCCCTGGATCAACCAATCGATGGTAG 1046
QY 980 TCCCTCAAAACCCCACTGCACACCAAGCCCGGCTCTGAAGGAGGACAAGGAGCGTGGGAGG 1039
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1047 TGCCACAGACCCCACTCCACACGGCCCGAGTGTGCAGGAGGACAAAGACCACTGGGACG 1106
QY 1040 ATGTCAAGGAGGAGATGACCAAGTGCCTTGGCCACAATCGCGTTGACTACGACGATCA 1099
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1107 AAGTCAAGGAGGAGATGACCAAGTGCCTTGGCCACTATGCGGGTAGACTACGACCAAGTGA 1166
QY 1100 AGATAAAAGATTGAAGATGCATCCAAACCCCTCTGCTGCTGAAGAGCGGGAAGAA 1154
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1167 AGATCAAGGACCTGAAGACCTCTAACAACCGGCTCCTCAACAAGAGGAGAGAAAAA 1221

RESULT 6
US-09-142-551A-1
; Sequence 1, Application US/09142551A
; Patent No. 6218136
; GENERAL INFORMATION:
; APPLICANT: KUMAR, SANJAY
; APPLICANT: LIVI, GEORGE P.
; APPLICANT: MCLAUGHLIN, MEGAN M.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: METHODS OF THE IDENTIFICATION OF
; TITLE OF INVENTION: PHARMACEUTICALLY ACTIVE COMPOUNDS
; FILE REFERENCE: P50448
; CURRENT APPLICATION NUMBER: US/09/142,551A
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US97/04256
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,286
; PRIOR FILING DATE: 1996-03-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1333
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-142-551A-1

Query Match 44.3%; Score 528; DB 3; Length 1333;
Best Local Similarity 71.7%; Pred. No. 1.4e-113;
Matches 736; Conservative 0; Mismatches 280; Indels 10; Gaps 3;

QY 140 GCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAAGGTCAACAGCCAGGTCTCTGG 199
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
129 GCGCGGAGCCCAAGAGTACGCGAGTACGCGACCGACGACTACCAGTTGTCCAAGCAGGTGCTGG 188
QY 200 GGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAGAGGACCCAGGAGAAATTCG 259
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
189 GCCTGGGTGTGAACGGCAAGTGTCTGGAGTGTCTCCATCGGCGCACTGGACAGAAGTGTG 248
QY 260 CCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAGGTGGAGCTGCACGTGGCGGG 319
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
249 CCCTGAAGTCTCTGTATGACAGCCCAAGGCCCGGAGGAGGTAGACCATCACTGGCAGG 308
QY 320 CCTCCCAGTGCCTGGCAGATCGTACGGATCGTGGATGTGTACGAGAAATCTGTACGCAGGGA 379
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
309 CTTCTGGCGGCCCCCATATTGTCTGCATCTCTGGATGTGTATGAGAAACATGCACCATGGCA 368
QY 380 GGAAGTGCCTGCTGATTGTTCATGGAATGTTTGGACGGTGGAGAACTCTTTAGCCGAATCC 439
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
369 AGCGTGTCTCTCATCATCATGGAATGCATGGAAGGTGGAAGGTGGTGGTGTTCAGCAGGATTC 428
QY 440 AGGATCGAGGAGACCGGCAATTCACAGAAAAGAGAAGCATCCGAAATCATGAAGAGCATCG 499
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
429 AGGAGCGTGGCGACCGAGGCTTTCATGAGAGAGAAGCTGCAGAGATAATGCGGGATATTG 488

QY	363	GAATCTGTAACGACGGAGGAAAGTGCGCTGCTGATTGTTCATGGAATGTTTGGACGGTGGAGA	422
Db	383	TGACATCTATGAGAGTGGGGGCCACCTCTACCTCATCATGACGTGGTGTCTGGGTGGGA	442
QY	423	ACTCTTTAGCGGAATCCAGGATCGAGGAGACCGGCATTACAGAAAGAGAAGCATCCGA	482
Db	443	GCTCTTTGACCGTATTGTGGAAGGCTTCTA-----CACGGAGCGGACGCCAGCCG	496
QY	483	AATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCATCG	542
Db	497	CCTCATCTTCCAGGTGCTGGATGCTGTGAAATACCTGTCATGACCTGGGCATTGTACACCG	556
QY	543	GGATGTCAGCCTGAGAAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAACT	602
Db	557	GGATCTCAAGCCAGAGAAATCTGCTGTACTACAGCTGGATGAAGACTCCAAAATCATGAT	616
QY	603	CACGTACTTTGGCTTTGGCCAAGGAAACCAACGACCAACACTCTTTGACCACTCCTTGTTA	662
Db	617	CTCCGACTTTGGCCTCTCCAAGATGGAGGACCCGGGCAGTGTGCTCTCCACCGCCTGTGG	676
QY	663	TACACCGTACTATGTGGCTCCAGAAGTGTCTGGGTCCAGAGAAAGTATGACAAAGTCCTGTGA	722
Db	677	AACCTCCGGGATACGTGGCCCTGAAAGTCCTGGCCCAAGAGCCCTACAGCAAGGCTGTGGA	736
QY	723	CATGTGTGCCCTGGGTGTCTATCATGTACATCCTGCTGTGTGGGTATCCCCCTTCTACTC	782
Db	737	TTGCTGTGTCCATAGGTGTCTATCGCCTACATCTTGCTGTGGGTACCTCCTTCTATGA	796
QY	783	CAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTATGA	842
Db	797	CGAGAATGATGCCAAACTCTTT-----GAACAGATTTTGAAGGCCGAGTACGA	844
QY	843	ATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAATCT	902
Db	845	GTTTGACTCTCCTTACTGGGACGACATCTCTGACTCTGCCAAAGATTTCATCCGGCACTT	904
QY	903	GCTGAAAACAGAGCCCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCCACCTTGGAT	962
Db	905	GATGGGAAGGACCCAGAGAAAAGATTACACCTGTGAGCAGGCCCTTGAGCAGCCCATGGAT	964

RESULT 9

US-09-949-016-1591
; Sequence 1591, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1591
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1591

RESULT 10
US-09-579-664B-3
; Sequence 3, Application US/09579664B
; Patent No. 6514719
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AN

Db 564 CCGGATCTCAAGCCAGAGAACTGCTGTACTACAGCCTGGATGAAGACTCCAAAATCAT 623
QY 600 ACTCACTGACTTTGGCTTTGCCAAGGAAACCAACAGCCACAACTCTTTTGACCACCTCCTTG 659
Db 624 GATCTCCGACTTTGGCCTCTCCAAGATGGAGGACCCGGCGAGTGTCTCTCCACCGCCTG 683
QY 660 TTATACACCGTACTATGTGGCTCCAGAAGTGTGGGTCCAGAGAAGTATGACAAAGTCCCTG 719
Db 684 TGGAACTCCGGGATACGTGGCCCCCTGAAGTCTTGCCCCAGAGCCCTACAGCAAGGCTGT 743
QY 720 TGACATGTGCTCCCTGGGTGTCAATCATGTACATCCTGCTGTGTGGGTATCCCCCCTTCTA 779
Db 744 GGATTGCTGCTCATAGGTGTCAATCGCCTACATCTTGCTCTGCGGTACCCCTCCCTTCTA 803
QY 780 CTCCAACCCGCGCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTA 839
Db 804 TGACGAGATGATGCCAAACTCTTT-----GAACAGATTTGAAGGCCGAGTA 851
QY 840 TGAATTTCCAAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAA 899
Db 852 CGAGTTTGACTCTCTTACTTGGGACGACATCTCTGACTCTGCCAAAGATTTTCATCCGGCA 911
QY 900 TCTGCTGAAAACAGAGCCCAACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCTTG 959
Db 912 CTTGATGGAGAAGGACCCAGAGAAAAGATTACCTGTGAGCGGCCTTGACGACACCCCATG 971
QY 960 GAT 962
Db 972 GAT 974

RESULT 14
US-08-878-989-12
; Sequence 12, Application US/08878989
; Patent No. 5885803
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,989
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:

; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1282 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSNOT06
; CLONE: 827431
US-08-878-989-12
Query Match 10.1%; Score 120.4; DB 2; Length 1282;
Best Local Similarity 50.3%; Pred. No. 1.9e-18;
Matches 416; Conservative 0; Mismatches 387; Indels 24; Gaps 4;
QY 142 CTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAAGTCAACAGGACCCAGGCCAGGTCCCTGGGG 201
Db 207 CTGCTGAAGAAACACACCGGAGACATCAGCAGCGTCTACGAGATCCGCGAGAGGCTCGGC 266
QY 202 CTGGCATCAACGGCAAAGTTTGCAGATCTTCAACAAGAGAGACCCAGGAGAAATTCGCC 261
Db 267 TCGGTGCTCTCTCCGAGGTGTGTGGCCAGGAGCGGGCTCCGACACACCTCGTGGCC 326
QY 262 CTCAA--AAATGCTTCAGGACTGCCCCAAGGCCCGCAGGAGGTGGAGCTGCACCTGGCG 318
Db 327 CTCAGTGCATCCCCAAGAAGGCCCTCCGGGGCAAGGAGGCCCTGGTGAGAACGAGATC 386
QY 319 GCCTCCAGTGCCTGATGTTGTCAGGATCGTGGATGTGTACGAGAAATCTGTACGAGGG 378
Db 387 GCAGTGCTCCGTAGGATCAGTCAACCCCAACATCGTCGCTCTGGAGGATGTCCACGAGAGC 446
QY 379 AGGAAGTGCCTGCTGATTGTCATGGAATGTTTGGACGGTGGAGAACTCTTTAGCCGAATC 438
Db 447 CCTTCCACCTCTACCTGGCCATGGAACCTGGTGACGGGTGGCGAGCTGTTTGACCGCATC 506
QY 439 CAGGATCGAGGAGACCAAGCAATTCACAGAAAGAGAAAGCATCCGAAATCATGAAGAGCATC 498
Db 507 ATGGAGCGCGG-----CTCCTACACAGAGAAGGATGCCAGCCATCTGGTGGGTCAAGTTC 560
QY 499 GGTGAGGCCATCCAGTATCTGCATTCAAATCAACATTTGCCATCGGGATGTCAAGCCTGAG 558
Db 561 CTTGGCGCGCTCTCCTACCTGCACAGCCTGGGGATCGTGACCGGCCCTGGGATATGTG 620
QY 559 AATCTCTTATACACCTCCAAAAGGCCCAACGCCATCTTGAAACTCACTGACTTTGGCTTT 618
Db 621 AACCTCCTGTATGCCACGCCCTTTGAGGACTCGAAGATCATGTCTCTGACTTTGGACTC 680
QY 619 GCCAAGGAAACCAACAGCCACAACTCTTTGACCACTCTCTTGTATACACCGTACTATGIG 678
Db 681 TCCA---AAATCCAGGCTGGGAACATGCTAGGCACCGCCTGTGGGACCCCTGGATATGTG 737
QY 679 GCTCCAGAAGTGTGGGTCCAGAGAAGTATGACAAGTCTCTGTGACATGTGGTCCCTGGGT 738
Db 738 GCCCAGAGCTCTTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGGCCCTGGGC 797
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QY 799 ATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTATGAATTTCCCAACCCAGAA 858
Db 858 CTCT-----TCAGCCAGATCTCTGAGGGCCAGCTATGAGTTTGACTNTCCTTTC 905
QY 859 TGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAATCTGCTGAAAAACAGAGCCC 918
Db 906 TGGGATGACATCTCAGAATCAGGCAAAAGACTTTATTCCGGCACCTTCTTGAGCGAGACCTT 965
QY 919 ACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCCCTTGGATCAT 965
Db 966 CAGAAGAGGTTTACCTGCCAACAGGCCCTTGCGGGACCTTTGGATCTT 1012

US-09-272-796-12
; Sequence 12, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1282 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSNOT06
; CLONE: 827431
US-09-272-796-12

Query Match 10.1%; Score 120.4; DB 3; Length 1282;
Best Local Similarity 50.3%; Pred. No. 1.9e-18;
Matches 416; Conservative 0; Mismatches 387; Indels 24; Gaps 4;
QY 142 CTGCAGATCAAGAAACGCCCATCATCGATGACTACAAGGTCAACGAGGTCAACGAGGTCTCCTGGGG 201
Db 207 CTGCTGAAGAAACACACGGAGGACATCAGCAGCGTCTACGAGATCCGCGAGAGGCTCGGC 266
QY 202 CTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAGAGGACCCAGGAAATTCGCC 261
Db 267 TCGGGTGCCTTCTCCGAGGTGGTGTCTGGCCCCAGGAGCGGGCTCCGCACACCTCGTGGCC 326
QY 262 CTCAA--AATGCTTCAGGACTGCCCCAGGCCCGCAGGGAGGTGGAGTGCACGTGGCG 318
Db 327 CTCAAGTGCATCCCCAAGAGGCCCTCCGGGGCAAGGAGGCCCTGGTGGAGAACGAGATC 386
QY 319 GCCTCCAGTCCCGCACATCGTACGGATCGTGGATGTGTACGAGATCTGTACGCAGGG 378
Db 387 GCAGTGTCCGTAGGATCAGTCAACCCCAACATCGTCTGTGGAGGATGTCCACGAGAGC 446
QY 379 AGGAAGTGCCTGCTGATTGTCTATGGAATGTTTGGACGGTGGAGAACTCTTTAGCCGAATC 438

Db 447 CCTTCCACCTCTACCTGGCCATGGAACCTGGTGACGGGTGGCGAGCTGTTTGACCGCATC 506
QY 439 CAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGAGCATCCGAAATCATGAAGAGCATC 498
Db 507 ATGGAGCGCG-----CTCCTACACAGAGAGAGGATGCCAGCCATCTGGTGGTCAGGTC 560
QY 499 GGTGAGGCCATCCAGTATCTGCAATCAATCAACATTCGCCCATCGGGATGTCAAGCCTGAG 558
Db 561 CTGGCGCCGTCTCCTACTGACAGCCCTTGGGATCGTGACCGGACCTCAAGCCCGAA 620
QY 559 AATCTCTTATACACCTCCAAAAGGCCCAACGCCCATCTTGAACCTCTGAAACTCACTGACTTTGGCTT 618
Db 621 AACCTCCTGTATGCCACGCCCTTTGAGGACTCGAAGATCATGGTCTCTGACTTTGGACTC 680
QY 619 GCCAAGGAAACCACACGCCACAACTCTTTGACCACTCCTTGTATATACACCGTACTATGTG 678
Db 681 TCCA---AAATCCAGGCTGGGAACATGCTAGGCACCGCCTGTGGGACCCCTGGATATGTG 737
QY 679 GCTCCAGAAAGTCTGGGTCCAGAGAAATATGACAAGTCTCTGTGACATGTGTCCTGGGT 738
Db 738 GCCCCAGAGCTTTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGGCCCTGGGC 797
QY 739 GTCATCATGTATCCTCTGTGTGGGTATCCCCCTTCTACTCCAACCCAGGCTTGCC 798
Db 798 GTCATCTCCTACATCCTGTGTGGGTACCCCTTCTACGACGAGAGCGAGCCCTGAG 857
QY 799 ATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTATGAATTTCCCAACCCAGAA 858
Db 858 CTCT-----TCAGCCAGATCCTGAGGSCCAGCTATGAGTTTGACTNTCCTTTC 905
QY 859 TGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAATCTGCTGAAACAGAGCCCC 918
Db 906 TGGGATGACATCTCAGAATCAGGCAAGACITTTATTGGGCACCTTCTGGAGCGAGACCTT 965
QY 919 ACCCAGAGAATGACCATCACCGAGTTTATGAACCCACCCCTTGGATCAT 965
Db 966 CAGAAGAGGTTTCACTGCCAACAGGCCCTTGGCGGACCTTTGGATCTT 1012

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OM_nucleic - nucleic search, using sw model

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(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 290227 seqs, 117694381 residues

Total number of hits satisfying chosen parameters: 580454

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Description
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2	1048.4	88.0	Sequence 1, Appli
3	555.8	46.7	Sequence 626, App
4	405.6	34.1	Sequence 2938, Ap
5	93	7.8	Sequence 2931, Ap
6	90.8	7.6	Sequence 350, App
7	88.2	7.4	Sequence 78535, A
8	85.4	7.2	Sequence 76461, A
9	83	7.0	Sequence 22824, A
10	81.4	6.8	Sequence 891, App
11	81.2	6.8	Sequence 3295, Ap
12	80.8	6.8	Sequence 781, App
13	80.8	6.8	Sequence 21986, A
14	79.8	6.7	Sequence 35, Appli
15	79.8	6.7	Sequence 3, Appli
16	78.6	6.6	Sequence 40, Appli
17	78.6	6.6	Sequence 41, Appli
18	77.6	6.5	Sequence 63, Appli
19	76.8	6.4	Sequence 20013, A
20	76	6.4	Sequence 18743, A
21	74.8	6.3	Sequence 26866, A
22	73.2	6.1	Sequence 27864, A
23	70	5.9	Sequence 33, Appli
24	69.6	5.8	Sequence 15987, A
25	69.6	5.8	Sequence 4590, Ap

c	26	68	5.7	1719	6	US-10-449-902-12406	Sequence 12406, A
	27	67.8	5.7	2044	6	US-10-449-902-23950	Sequence 23950, A
	28	67.8	5.7	2313	6	US-10-449-902-18961	Sequence 18961, A
	29	67.6	5.7	2127	6	US-10-449-902-26500	Sequence 26500, A
	30	63.4	5.3	2563	6	US-10-449-902-24216	Sequence 24216, A
	31	63.4	5.3	2696	6	US-10-449-902-18862	Sequence 18862, A
	32	62	5.2	1968	6	US-10-449-902-20206	Sequence 20206, A
	33	61	5.1	1160	6	US-10-449-902-609	Sequence 609, App
	34	60.8	5.1	2173	6	US-10-449-902-25032	Sequence 25032, A
	35	60.6	5.1	2365	6	US-10-449-902-17898	Sequence 17898, A
	36	59.6	5.0	2343	6	US-10-473-173-6	Sequence 6, Appli
	37	59.6	5.0	2386	6	US-10-505-928-846	Sequence 846, App
	38	59	5.0	1764	6	US-10-953-349-903	Sequence 903, App
	39	59	5.0	2163	6	US-10-449-902-7754	Sequence 7754, Ap
	40	57.4	4.8	2343	6	US-10-449-902-26016	Sequence 26016, A
	41	57.2	4.8	900	7	US-11-217-529-81431	Sequence 81431, A
	42	56	4.7	1112	6	US-10-953-349-33546	Sequence 33546, A
	43	56	4.7	2392	6	US-10-449-902-18001	Sequence 18001, A
	44	55	4.6	2444	6	US-10-449-902-26044	Sequence 26044, A
	45	54.2	4.6	1594	6	US-10-449-902-16926	Sequence 16926, A

ALIGNMENTS

RESULT 1
US-11-273-567-2
; Sequence 2, Application US/11273567
; Publication No. US20060115453A1
; GENERAL INFORMATION:
; APPLICANT: Yaffe, Michael B.
; APPLICANT: Manke, Isaac A.
; APPLICANT: Reinhardt, Hans Christian
; APPLICANT: Lim, Daniel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING CELLULAR PROLIFERATIVE
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: 01997/557002
; CURRENT APPLICATION NUMBER: US/11/273,567
; CURRENT FILING DATE: 2005-11-14
; PRIOR APPLICATION NUMBER: 60/627,352
; PRIOR FILING DATE: 2004-11-12
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 3071
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-273-567-2

Query Match				99.9%;	Score 1189.4;	DB 7;	Length 3071;
Best Local Similarity				99.9%;	Pred. No. 6.3e-235;		
Matches 1190;				Conservative	0;	Mismatches	1;
						Indels	0;
						Gaps	0;
Qy	1	TCCCAGGGCCAGAGCCCGCGTTC	1	TCCCAGGGCCAGAGCCCGCGTTC	1	TCCCAGGGCCAGAGCCCGCGTTC	1
Db	299	TCCCAGGGCCAGAGCCCGCGTTC	299	TCCCAGGGCCAGAGCCCGCGTTC	299	TCCCAGGGCCAGAGCCCGCGTTC	299
Qy	61	ACCCCTGCCCTGCCGACCCCGCG	61	ACCCCTGCCCTGCCGACCCCGCG	61	ACCCCTGCCCTGCCGACCCCGCG	61
Db	359	ACCCCTGCCCTGCCGACCCCGCG	359	ACCCCTGCCCTGCCGACCCCGCG	359	ACCCCTGCCCTGCCGACCCCGCG	359
Qy	121	CAGTTCACGTCAGTCCGGCTTC	121	CAGTTCACGTCAGTCCGGCTTC	121	CAGTTCACGTCAGTCCGGCTTC	121
Db	419	CAGTTCACGTCAGTCCGGCTTC	419	CAGTTCACGTCAGTCCGGCTTC	419	CAGTTCACGTCAGTCCGGCTTC	419
Qy	181	GTCACGACCCAGGTCCTGGGG	181	GTCACGACCCAGGTCCTGGGG	181	GTCACGACCCAGGTCCTGGGG	181
Db	479	GTCACGACCCAGGTCCTGGGG	479	GTCACGACCCAGGTCCTGGGG	479	GTCACGACCCAGGTCCTGGGG	479
Qy	241	AGGACCCAGGAGAAATTCGCC	241	AGGACCCAGGAGAAATTCGCC	241	AGGACCCAGGAGAAATTCGCC	241
Db	539	AGGACCCAGGAGAAATTCGCC	539	AGGACCCAGGAGAAATTCGCC	539	AGGACCCAGGAGAAATTCGCC	539

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QY 301 GTGGAGCTGCACTGGCGGGCCCTCCACGTGCCCGCACATCGTACGGATCGTGGATGTGTAC 360
|||
Db 599 GTGGAGCTGCACTGGCGGGCCCTCCACGTGCCCGCACATCGTACGGATCGTGGATGTGTAC 658

QY 361 GAGAACTCTGACCGCAGGGAGGAAGTGCCCTGCTGATTGTTCATGGAAATGTTTGGACGGTGA 420
|||
Db 659 GAGAACTCTGTACGACGGGAGGAAGTGCCCTGCTGATTGTTCATGGAAATGTTTGGACGGTGA 718

QY 421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGAAGCATCC 480
|||
Db 719 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGAAGCATCC 778

QY 481 GAAATCATGAAGACATCGGTGAGGCCATCCAGTATCTGCAATTCATCAACATTTGCCCAT 540
|||
Db 779 GAAATCATGAAGACATCGGTGAGGCCATCCAGTATCTGCAATTCATCAACATTTGCCCAT 838

QY 541 CGGGATGTCAAGCCTGAGAAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 600
|||
Db 839 CGGGATGTCAAGCCTGAGAAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 898

QY 601 CTCACTGACTTTGGCTTTGCCAAGGAAACACACAGCCCAAACTCTTTGACCACTCCTTGT 660
|||
Db 899 CTCACTGACTTTGGCTTTGCCAAGGAAACACACAGCCCAAACTCTTTGACCACTCCTTGT 958

QY 661 TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCCTGT 720
|||
Db 959 TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCCTGT 1018

QY 721 GACATGTGGTCCCTGGGTGTTCATCATGTATACATCTGCTGTGTGGGTATCCCCCTTCTAC 780
|||
Db 1019 GACATGTGGTCCCTGGGTGTTCATCATGTATACATCTGCTGTGTGGGTATCCCCCTTCTAC 1078

QY 781 TCCAAACCAACCGCCTTGCCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCCAGTAT 840
|||
Db 1079 TCCAAACCAACCGCCTTGCCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCCAGTAT 1138

QY 841 GAATTTCCCAACCCAGAAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
|||
Db 1139 GAATTTCCCAACCCAGAAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1198

QY 901 CTGCTGAAAAACAGAGCCCCACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCTTGG 960
|||
Db 1199 CTGCTGAAAAACAGAGCCCCACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCTTGG 1258

QY 961 ATCATGCAATCAACAAAGGTCCCTCAAAACCCACTGCACACCGCCGGTCTGAAAGGAG 1020
|||
Db 1259 ATCATGCAATCAACAAAGGTCCCTCAAAACCCACTGCACACCGCCGGTCTGAAAGGAG 1318

QY 1021 GACAAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCATGCCCTTTGGCCACAATGCGC 1080
|||
Db 1319 GACAAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCATGCCCTTTGGCCACAATGCGC 1378

QY 1081 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAAACCTCTGCTGCTG 1140
|||
Db 1379 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAAACCTCTGCTGCTG 1438

QY 1141 AAGAGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCCACTGA 1191
|||
Db 1439 AAGAGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCCACTGA 1489
```

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RESULT 2
US-11-273-567-1
; Sequence 1, Application US/11273567
; Publication No. US20060115453A1
; GENERAL INFORMATION:
; APPLICANT: Yaffe, Michael B.
; APPLICANT: Manke, Isaac A.
; APPLICANT: Reinhardt, Hans Christian
; APPLICANT: Lim, Daniel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING CELLULAR PROLIFERATIVE
; DISEASES
; FILE REFERENCE: 01997/557002
```

```
; CURRENT APPLICATION NUMBER: US/11/273,567
; CURRENT FILING DATE: 2005-11-14
; PRIOR APPLICATION NUMBER: 60/627,352
; PRIOR FILING DATE: 2004-11-12
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 3608
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-273-567-1

Query Match      88.0%; Score 1048.4; DB 7; Length 3608;
Best Local Similarity 99.9%; Pred. No. 4.6e-206;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCACAGGCCAGAGCCCCCGCGGTGCCGTTCCCCCGCCCCCGCGCCCCCGCGCAGCCCCC 60
Db 299 TCCACAGGCCAGAGCCCCCGCGGTGCCGTTCCCCCGCCCCCGCGCCCCCGCGCAGCCCCC 358

QY 61 ACCCTGCTGCTGCCGACACCCCCCGCGCAGCCCGCGCCCCCGCGCAGCAGTTCCCCG 120
Db 359 ACCCTGCTGCTGCCGACACCCCCCGCGCAGCCCGCGCCCCCGCGCAGCAGTTCCCCG 418

QY 121 CAGTTCACGTCAAAGTCGGGCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 180
Db 419 CAGTTCACGTCAAAGTCGGGCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 478

QY 181 GTCACAGCCAGGTCTCTGGGGTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG 240
Db 479 GTCACAGCCAGGTCTCTGGGGTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG 538

QY 241 AGGACCCAGGAGAAATTCGCCCTCAAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 300
Db 539 AGGACCCAGGAGAAATTCGCCCTCAAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 598

QY 301 GTGAGCTGCACGTGGCGGCCCTCCAGTGCCTCCGCACATCGTACGGATCGTGGATGTGTAC 360
Db 599 GTGAGCTGCACGTGGCGGCCCTCCAGTGCCTCCGCACATCGTACGGATCGTGGATGTGTAC 658

QY 361 GAGAATCTGTACGCGAGGAGGAAGTGCTGCTGATTGTTCATGGAATGTTTGGACGGTGA 420
Db 659 GAGAATCTGTACGCGAGGAGGAAGTGCTGCTGATTGTTCATGGAATGTTTGGACGGTGA 718

QY 421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGAAGCATCC 480
Db 719 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGAAGCATCC 778

QY 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCAATTCATCAACATTTGCCCAT 540
Db 779 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCAATTCATCAACATTTGCCCAT 838

QY 541 CGGGATGTCAAGCCTGAGAAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 600
Db 839 CGGGATGTCAAGCCTGAGAAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 898

QY 601 CTCACTGACTTTGGCTTTGCCAAGGAAACACACAGCCCAAACTCTTTGACCACTCCTTGT 660
Db 899 CTCACTGACTTTGGCTTTGCCAAGGAAACACACAGCCCAAACTCTTTGACCACTCCTTGT 958

QY 661 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAGTATGACAAGTCCTGT 720
Db 959 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAGTATGACAAGTCCTGT 1018

QY 721 GACATGTGGTCCCTGGGTGTTCATCATGTATACATCTGCTGTGTGGGTATCCCCCTTCTAC 780
Db 1019 GACATGTGGTCCCTGGGTGTTCATCATGTATACATCTGCTGTGTGGGTATCCCCCTTCTAC 1078

QY 781 TCCAAACCAACCGCCTTGCCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCCAGTAT 840
Db 1079 TCCAAACCAACCGCCTTGCCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCCAGTAT 1138

QY 841 GAATTTCCCAACCCAGAAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
Db 1139 GAATTTCCCAACCCAGAAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1198

QY 901 CTGCTGAAAAACAGAGCCCCACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCTTGG 960
Db 1199 CTGCTGAAAAACAGAGCCCCACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCTTGG 1258

QY 961 ATCATGCAATCAACAAAGGTCCCTCAAAACCCACTGCACACCGCCGGTCTGAAAGGAG 1020
Db 1259 ATCATGCAATCAACAAAGGTCCCTCAAAACCCACTGCACACCGCCGGTCTGAAAGGAG 1318

QY 1021 GACAAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCATGCCCTTTGGCCACAATGCGC 1080
Db 1319 GACAAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCATGCCCTTTGGCCACAATGCGC 1378

QY 1081 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAAACCTCTGCTGCTG 1140
Db 1379 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAAACCTCTGCTGCTG 1438

QY 1141 AAGAGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCCACTGA 1191
Db 1439 AAGAGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCCACTGA 1489
```

Db 1139 GAATTTCCCAACCCAGAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1198
QY 901 CTGCTGAAACACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGG 960
Db 1199 CTGCTGAAACACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGG 1258
QY 961 ATCATGCAATCAACAAAGGTCCTCAAAACCCCACTGCACACCCAGCCGGGTCCTGAAGGAG 1020
Db 1259 ATCATGCAATCAACAAAGGTCCTCAAAACCCCACTGCACACCCAGCCGGGTCCTGAAGGAG 1318
QY 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAG 1050
Db 1319 GACAAGGAGCGGTGGGAGGATGTCAAGGGG 1348

RESULT 3
US-10-505-928-626
; Sequence 626, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 626
; LENGTH: 2509
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-626

Query Match 46.7%; Score 555.8; DB 6; Length 2509;
Best Local Similarity 72.4%; Pred. No. 2.4e-105;
Matches 735; Conservative 0; Mismatches 277; Indels 3; Gaps 1;
QY 140 GCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAGGTACACGACCCAGGTCTCTGG 199
Db 210 GCGGGAGCCCAAGAAAGTACGCAGTACCGGAGCTACCAGTTGTCCAAAGCAGGTGCTGG 269
QY 200 GGCTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAGAGGACCCAGGAGAAATTCG 259
Db 270 GCCTGGGTGTGAACGGCAAAAGTGTCTGGAGTGTCTCCATCGCGCACTGGACAGAAGTGTG 329
QY 260 CCCTCAAAATGTTTCAGGACTGCCCCCAAGSCCGCAGGAGGTGGAGTGCACCTGGCGGG 319
Db 330 CCCTGAAGCTCTGTATGACAGCCCCCAAGSCCGCAGGAGGTAGACCATCACTGGCAGG 389
QY 320 CCTCCAGTGCCTCCGCACATCGTACGGATCTGGATGTGTACGAGAACTGTGTACGCAGGGA 379
Db 390 CTCTCTGGCGCCCCCATATTGTCTGCATCCTGGATGTGTATGAGAACTATGCACCATGGCA 449
QY 380 GGAAGTGCCTGCTGATTGTATGGAATGTTTGGACGGTGGAGAACTCTTTAGCCGAATCC 439
Db 450 AGCGTGTCTCCTCATCATCATGGAATGCATGGAAGGTGGTGGTGTGTTTTCAGCAGGATTC 509
QY 440 AGGATCGAGGAGACCAAGGCATTCACAGAAAGAGAGCATCCGAAATCATGAAGAGCATCG 499
Db 510 AGGAGCGTGGCGACCAAGGCTTTCACTGAGAGAGAAAGTGCAGAGATAATGCGGGATATTG 569
QY 500 GTGAGGCCCATCCAGTATCTGCATTCAATCAACATATGCCCATCGGGATGTCAAGCCTGAGA 559
Db 570 GCACTGCCATCCAGTTTCTGCACAGCCATAACATTGCCACCCGAGATGTCAAGCCTGAAA 629
QY 560 ATCTCTTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAACTCACTGACTTTGGCTTTG 619
Db 630 ACCTACTCTACACATCTAAGGAGAAAGACCGAGTGTCTTAAGCTCACCGATTTTGGCTTTG 689
QY 620 CCAAGGAACCAACCAAGCCACAACCTCTTTGACCACTCCTTGTATTATACCCGTACTATGTGG 679

Db 690 CTAAGGAGACCAC- --CCAAATGCCCTGCAGACACCCCTGCTATACTCCTATTATGTGG 746
QY 680 CTCCAGAAAGTCTGGGTCCAGAGAAAGTATGACAAAGTCTCTGTGACATGTGGTCCCTGGGTG 739
Db 747 CCCCTGAGGTCTCTGGGTCCAGAGAAAGTATGACAAAGTCAATGTGACATGTGGTCCCTGGGTG 806
QY 740 TCATCATGTACATCCTCTGTGTGTGGGTATCCCCCTTCTACTCCAACACAGGCGCTTGCCA 799
Db 807 TCATCATGTACATCCTCTTTGTGGCTTCCCAACCTTCTACTCCAACACAGGCGCCAGGCCA 866
QY 800 TCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTATGAATTTCCCAACCCAGAAT 859
Db 867 TCTCCCCGGGATGAAGAGGAGGATTTCGCTGGGCGCAGTACGGCTTCCCCAATCCTGAGT 926
QY 860 GGTCAAGATATCAGAGGAAGTGAAGATGCTCATTCGGAATCTGCTGAAAAACAGAGCCCA 919
Db 927 GGTCAAGATCTCTGAGGATGCCAAGCAGCTGATCCGCCCTCCTGTTGAAGACAGACCCCA 986
QY 920 CCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGGATCATGCAATCAACAAAG 979
Db 987 CAGAGAGGCTGACCATCACTCAGTTTCATGAACCAACCCCTGGATCAACCAATCGATGGTAG 1046
QY 980 TCCCTCAAAACCCCACTGCACACCGCGGTCTTGAAGGAGGACAAAGAGCGGTGGGAGG 1039
Db 1047 TGCCACAGACCCCACTCCACACGCGCCGAGTGTGCAGGAGGACAAAGACCACTGGGACG 1106
QY 1040 ATGTCAAGGAGGAGATGACCAGTGCCTTGGCCACAATGCGCGTTGACTACGAGCAGATCA 1099
Db 1107 AAGTCAAGGAGGAGATGACCAGTGCCTTGGCCACTATGCGGGTAGACTACGACCAGGTGA 1166
QY 1100 AGATAAAAAAGATTGAAGATGCATCCAACCCCTCTGCTGCTGAAGAGCGGGAAGAA 1154
Db 1167 AGATCAAGGACCTGAAGACCTCTTAACAACCCGGCTCCTCAACAAGAGGAGAAAAA 1221

RESULT 4
US-10-488-619-2938
; Sequence 2938, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations v
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2938
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2938

Query Match 34.1%; Score 405.6; DB 6; Length 574;
Best Local Similarity 91.7%; Pred. No. 9.2e-75;
Matches 429; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
QY 724 ATGTGGTCCCTGGGTGTCATCATGTACATCCTGTGTGTGGGTATCCCCCTTCTACTCC 783
Db 1 ATGTGGTCTTGGGTGTCATCATGTATATTTTGTGTGTGGGTATCCCCCTTCTATTCC 60
QY 784 AACCAAGCCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTATGAA 843
Db 61 AATCAGGCGCTTGCCATCTCTCCGGGCATGAAGACTCGTATTGGAATGGGCCAGTATGAA 120
QY 844 TTTCCCAACCCAGAAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAATCTG 903
Db 121 TTTCTTAACCCGGATTGGTCAAGAAGTATCAGAAGAAGTGAAGATGCTTATCCGGAATCTG 180
QY 904 CTGAAAAACAGAGCCCAACCCAGAGAATGACCATCACCGAGTTTATGAACCCCTTGGATC 963

Db 181 CTA AAAACAGAGCCCAACCAGAGAGAAATGACCATCACAGAAATTCATGAACCAACCCCTGGATC 240

QY 964 ATGCAATCAACAAGGTCCTCAAACCCCACTGCACACCAGCCGGGTCTCTGAAGGAGGAC 1023

Db 241 ATGCAATCTACGAAGGTCCTCAGACTCCACTGCACACCAGCCGTCTCTGAAGGAGGAC 300

QY 1024 AAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTTGGCCACAATGCGCGTT 1083

Db 301 AAGGAACGATGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTTGGCCACGATCGGTGT 360

QY 1084 GACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACCCCTCTGCTGCTGAAG 1143

Db 361 GACTATGAGCAGATCAAGATAAAGAAGATAGAAGACGCATCCAACCCCTCTGCTTCTCAAG 420

QY 1144 AGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTTGCCCCACTGA 1191

Db 421 AGCGGAAGAAAGCTCGTGCTGTGGAGGATCGGGCTCTCGCCCCACTGA 468

RESULT 5

US-11-217-529-2931

; Sequence 2931, Application US/11217529

; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHIISA

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529

; CURRENT FILING DATE: 2005-09-02

; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02

; NUMBER OF SEQ ID NOS: 197023

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 2931

; LENGTH: 1329

; TYPE: DNA

; ORGANISM: Saccharomyces pastorianus

US-11-217-529-2931

Query Match 7.8%; Score 93; DB 7; Length 1329;

Best Local Similarity 51.9%; Pred. No. 9.8e-11;

Matches 263; Conservative 0; Mismatches 235; Indels 9; Gaps 2;

QY 459 ATTACAGAAAAGAAAGCATCCGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCT 518

Db 396 ATTCACTGAGGTGGATCGGTTGAGAAATCCTGTTGAGATTTTAAGCGCTGTCAAATACAT 455

QY 519 GCATTCAATCAACATGCCCCATCGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAA 578

Db 456 GCAC TCCAGAAATATGTTTCATAGGATTTAAAGCCAGAAAATTTGCTGTATAGATAT 515

QY 579 AAGGCCCCAACGCCATCTCTGAAACTCACTGACTTTGGCTTTGCCAAGGAAACCACCA 638

Db 516 AAGCGATGAATCTCCATTGGTGATCGCTGATTTTGGTATTGCCAAGAGGTTAAAGCGA 575

QY 639 CAACTCTTTTGAC----CACTCCTTGTTATACACCGTACTATGTGGCTCCAGAAGTGTGGG 695

Db 576 TGAGGAGCTCATTTACAAAGCAGCAGGTTTCGTTGGGTTATGTGGCCCCAGAAAGTGCTTAC 635

QY 696 TCCAGAGAAGTATGACAAAGTCCCTGTGACATGTGTCCTCGGTGTCTATCATGTACATCCT 755

Db 636 CCAAGATGGTCATGGTAAACCTTGTGATATTGGTCGATTGGTGTCATCACACATACGTT 695

QY 756 GCTGTGTGGGTATCCCCCTTCTACTCCAAACCACGGCCTTGCCATCTCTCCGGGCATGAA 815

Db 696 GCTGTGTGGCTATTCTGCATTCAAAGCTGAAAGAGTCATGGATTTCCCTTGACG-----A 749

QY 816 GACTCGCATCCGAATGGGCCAGTATGAATTTCCCAACCCAGAAATGGTCAGAAGTATCAGA 875

Db 750 GTGTACAACCGGGAAGTATCCACTGACATTTTCATCGGCCTTATTGGGATTCAGTATCTGA 809

QY 876 GGAAGTGAAGATGCTCATTCGGAATCTGCTGAAAAACAGAGCCCAAGAGAAATGACCAT 935

Db 810 TAAAGCTAAGCGATTTCATTTTGAAGCTCTTGATTTAGATCCCAACAAGAGGCCAACCGC 869

QY 936 CACCGAGTTTATGAACCAACCCCTTGGAT 962

Db 870 TGCAGAACTGTTGGAAGACCCCATGGAT 896

RESULT 6

US-10-505-928-350

; Sequence 350, Application US/10505928

; Publication No. US20060088532A1

; GENERAL INFORMATION:

; APPLICANT: Ludwig Institute for Cancer Research et al.

; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

; FILE REFERENCE: 28967/39178

; CURRENT APPLICATION NUMBER: US/10/505,928

; CURRENT FILING DATE: 2004-08-27

; PRIOR APPLICATION NUMBER: US 60/363,019

; PRIOR FILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: PatentIn 3.2

; SEQ ID NO 350

; LENGTH: 3982

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-505-928-350

Query Match 7.6%; Score 90.8; DB 6; Length 3982;

Best Local Similarity 49.3%; Pred. No. 3.6e-10;

Matches 453; Conservative 0; Mismatches 432; Indels 33; Gaps 7;

QY 87 GCAGCCGCGCGCGCCCGCCCGCAGAGTTCCTCCGAGTTCCACGTCGAAGTCCGGCCTGCA 146

Db 1382 GGAGCCCTCACAGCAAGATCTGCACAAAGTCCCAGTTCACCCCAATCGTGACAGTTACA 1441

QY 147 GATCAAGAAGAACGCCCATCATCGATGACTACAGGTCAACCAGCCAGGTCCTTGGGCTGGG 206

Db 1442 CGGGAACAACATCCACTTCACCGATGGCTACGAG--ATCAAGAGGACATCGGGGTGGG 1498

QY 207 CATCAACGGCAAAAGTTTTCAGATCTTCAACAAGAGGACCCAGGAGAAATTCGCCCTCAA 266

Db 1499 CTCCTACTCAGTGTGCAAGCGATGTGTGCATAAAGCCACAGACACCGAGTATGCCGTGAA 1558

QY 267 AATGCTTCAGGACTGCCCCAAAGGCCCGCAGG--GAGGTGGAGCTGCACCTGGCGGCCTC 323

Db 1559 GATCATTGATAAGAGCAAGAGAGACCCCTCGGAAGAGATTGAGATCTCTCTGCGGTACGG 1618

QY 324 CCAGTGCCCGCACATCGTACGGATCGTGGATGTGTACGAGAACTGTACGCGAGGGAGGAA 383

Db 1619 CCAGCACCCGGAACATCATCACCCCTCAAGGATGTCTATGATGAT-----GGCAA 1666

QY 384 GTGCCTGCTGATTGTCAATGGAATGTTTGGACGGTGGAGAACTCTTTAGCCGAATCCAGGA 443

Db 1667 GTTTGTGTACCTGGTAATGGAGCTGATCGTGGTGGGAGCTCCTGGACCGCATCCTCCG 1726

QY 444 TCGAGGAGACCAAGGCATTTCACAGAAAAGAGAACGATCCGAAATCATGAAGAGCATCGGTGA 503

Db 1727 GCAGAGATAC-----TTCTCGGAGCGCGAAGCCAGTGACGTCTCTGTGCACCATCACCAA 1780

QY 504 GGCCATCCAGTATCTGCATTCATCAATCAACATTTGCCCATCGGGATGTCAAGCCTGAGAACT 563

Db 1781 GACCATGGACTACCTCCATTTCCCAGGGGGTGTGTTTCATCGAGACCTGAAGCCGAGTAACAT 1840

QY 564 CTTATACACTCCAAAAGGCCCAACGCCAT---CCTGAAACTCACTGACTTTGGCTTTGC 620

Db 1841 CCTGTACAGGGATGAGTCGGGGAGCCCAAGAAATCCATCCGAGTCTGCGACTTCGGCTTTGC 1900

QY 621 CAAGGAAACCAACAGCCCAAACTCTTTTGACC---ACTCCTTGTTATACACCGTACTATGT 677

Db 1901 CAAGCAGCTGCGCGGGGAACGGGCTGCTCATGACACCCTGTACACGGCCAATTTCGT 1960
Qy 678 GGCTCCAGAAGTGTGGTCCAGAGAAAGTATGACAAAGTCTGTGACATGTGGTCCCTGGG 737
Db 1961 GGCCCCGGAGGTCTGAAGCGTCAAGGCTATGATCGCGGCTGTGACATCTGGAGTTTGGG 2020
Qy 738 TGTCAATGATACATCTCTGTGTGGGTATCCCCCTTCTACTCCAACCAACGGCCTTGC 797
Db 2021 GATCCTGTTGTACACCATGCTGGCAGGATTTACCCCTTTTGCAATGGGCCAGAC---GA 2077
Qy 798 CATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTATGAATTTCCCAACCCAGA 857
Db 2078 TACCCCTGAGGAGATTCTGGCGCGGATCGGCAGTGGGAAGTATGCCCTTTCTGGGGGAAA 2137
Qy 858 ATGGTCAAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAATCTGCTGAAAACAGAGCC 917
Db 2138 CTGGGACTCGATATCTGACGCAGCTAAAGACGTCGTGCCAAGATGCTCCACGTGGACCC 2197
Qy 918 CACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCCCTTGGATCATGCAATCAACAAA 977
Db 2198 TCATCAGCGCCTGACGGCGATGCAAGTGCTCAAAACACCCGTGGTGGTCAACAGAGTA 2257
Qy 978 GGTCCCTCAAAACCCCACT 995
Db 2258 CCTGTCCCCAAACCAGCT 2275

RESULT 7
US-11-217-529-78535
; Sequence 78535, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78535
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78535

Query Match 7.4%; Score 88.2; DB 7; Length 1344;
Best Local Similarity 49.9%; Pred. No. 9.5e-10;
Matches 312; Conservative 0; Mismatches 298; Indels 15; Gaps 3;
Qy 343 CGGATCGTGGATGTGTACGAGAACTCTGTACGAGGAGGAGGAGTGCCTGCTGATTGTCA 402
Db 316 CGGAACATTGTGTCATTCAAGGATTGGTTTGAATCGAAGGATAAGTTCTATATTGTCACT 375
Qy 403 GAATGTTTGGACGGTGGAGAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATT 462
Db 376 CAGCTGGCAACAGGAGGTGAATATTGTGATAGAATTCGTCTAGAGG-----GAAGTTC 429
Qy 463 ACAGAAAGAGAGCATCCGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCA 522
Db 430 ACAGAAGTGGATGCTGTGAAATCATAGTTCAAGATCTTGGTGCCGTGGAGTATATGCA 489
Qy 523 TCAATCAACATTTGCCCATCGGGATGTCAAGCCTGAGAATCTCTTTATACACCTCCAAAAG 582
Db 490 TCCAAGAATGTTTTCATAGAGATTTGAAACCTGAGAACGTTTGTATGTTGATAAGTCA 549

Qy 583 CCCAACGCCATCCTGAAACTCACTGACTTTGGCTTTGCCAAGGAAACCACCAGCCACAAC 642
Db 550 GAAATTCGCCCTCTGGTAATTGCGGACTTCGGTATAGCTAAACAATTGAAGGGGGAGAG 609
Qy 643 TCTTTGA---CCACTCCTTGTATTATACACCGTACTATGTGGCTCCAGAAAGTCTGGGTCCA 699
Db 610 GATTTGATATACAAAGCAGCCGGATCGTTGGGCTATGTGGCACCAGAAAGTCTCTCACAAA 669
Qy 700 GAGAAATATGACAAAGTCTGTGACATGTGGTCCCTGGGTGTATCATCATGTACATCCTGCTG 759
Db 670 GATGGACATGTTAAGCCTTGTGATATATGTTCCATTGGTGTGATCAATATCTTTACTG 729
Qy 760 TGTGGGTATCCCCCTTCTACTCTCAACCAACCGCCTTGCCATCTCTCCGGGCATGAAGACT 819
Db 730 TCGGGTTATTCTCTTTTATTGCGGAAGCGTTGAAGGATTCATGGAGGAATGTACAGCT 789
Qy 820 CGCATCCGAATGGGCCAGTATGAATTTCCCAACCAGAACCCAGAAATGGTCAGAAGTATCAGAGGAA 879
Db 790 TCGAGATA-----CCCGTAACCTTCCATATGCCATATTGGGATAACATATCTATTGAT 843
Qy 880 GTGAAGATGCTCATTCGGAATCTGCTGAAAAACAGAGCCCAACCCAGAGAATGACCATCACC 939
Db 844 GCCAAGCGTTTCATCTTGAAGGCATTGAGATTGAATCCAGCTGACAGACCAACTGCTACG 903
Qy 940 GAGTTTATGAACCAACCCCTTGGATCA 964
Db 904 GAATTGCTGGACGATCCATGGATTA 928

RESULT 8
US-11-217-529-76461
; Sequence 76461, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76461
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76461

Query Match 7.2%; Score 85.4; DB 7; Length 1341;
Best Local Similarity 50.9%; Pred. No. 3.5e-09;
Matches 259; Conservative 0; Mismatches 241; Indels 9; Gaps 2;
Qy 460 TTCACAGAAAAGAGAGCATCCGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTG 519
Db 397 TTCACTGAGGAAGATGCAGTGAGAATTTTGGTTGAAATATTGAGCGCAGTCAAATATATG 456
Qy 520 CATTCAATCAACATTGCCCCATCGGGATGTCAAGCCTGAGAATCTTTATACACCTCCAAA 579
Db 457 CATTCTCAGAAATATTGTTCATAGGACTTGAAACCGGAAAATTTATGTATATAGATAAA 516
Qy 580 AGGCCCAACGCCATCCTGAAACTCACTGACTTTGGCTTTGCCAAGGAAACCACCAGCCAC 639
Db 517 AGTGACGAATCTCCACTGTAGATAGTTGCTGATTTTGGTATCGCAAGAGATTGAAAAGTGAT 576
Qy 640 AACTCTTTTGACC---ACTCCTTTGTATACACCGTACTATGTGGCTCCAGAAGTGTGGGT 696
Db 577 GAGAACTCCTCTATAGCCCGCAGGCTCACTGGGTTACGTGGCTCCAGAGGTACTTACT 636

Db 678 ATGGAACCTGTGGATATCTGGCCCTGCGGGGTATCCTGTATATCCTCCTGGTGGGCT 737

QY 767 ATCCCCCTTCTACTCAACACCGGCTTGCCATCTCTCCGGGATGAAGACTCGCATCC 826

Db 738 ATCCTCCCTTCTGGGATGAGGATCAGCACAAGCTGTATCAGCAGATCAAGGCT----- 790

QY 827 GAATGGCCAGTATGAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGA 886

Db 791 -----GGAGCCTATGATTTCCCATCACCAAGTGGACACGGTAACCTCTGAAGCCCAAGA 845

QY 887 TGCTCATTCGGAATCTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTA 946

Db 846 ACTTGATCAACAGATGCTGACCATAAACCCAGCAAGCGCATCACGGCTGACCAGGCTC 905

QY 947 TGAACCACTTTGGATCATGCAATCAACAAAGGT 980

Db 906 TCAAGCACCCGTGGGTCTGTCAACGATCCACGGT 939

RESULT 13

US-10-449-902-21986

; Sequence 21986, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 21986

; LENGTH: 2641

; TYPE: DNA

; ORGANISM: Oryza sativa

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: AK072204

; DATABASE ENTRY DATE: 2001-12-06

US-10-449-902-21986

Query Match 6.8%; Score 80.8; DB 6; Length 2641;

Best Local Similarity 49.7%; Pred. No. 3.6e-08;

Matches 304; Conservative 0; Mismatches 287; Indels 21; Gaps 3;

QY 387 CCTGCTGATTGTCATGGAATGTTTGGACGGTGGAGAACTCTTTAGCCGAATCCAGGATCG 446

Db 1242 CGTGACCTCGTCATGGAGCTCTGCGCCGGCGCGAGCTGTTTCGACCGGATCGTCCAGAA 1301

QY 447 AGGAGACCGGCAATTCACAGAAAGAGAGCATCCGAAATCATGAAGAGCATCGGTGAGGC 506

Db 1302 GGGGCAC-----TACACGAGCGGAAGCGCGGAGCTCGCCAGGGTCATCGTCGGCGT 1355

QY 507 CATCCAGTATCTGCATTCAATCAACATTGCCATCGGGATGTCAAGCCTGAGAATCTCTT 566

Db 1356 CGTCGAGGTGTGCCACTCCATGGCGGTGATGACCCGTGATCTCAAGCCCGAGAACTTCCT 1415

QY 567 ATACACCTCCAAAGGCCCAACGCCATCCTGAAACTCACTGACTTTGGCTTTGCCAAGGA 626

Db 1416 CTTGCGCCGACACGAGGAGGCCGCTCTCAAGACCATTGACTTTGGTCTCTCCATTTT 1475

QY 627 AACCAACGACCAACTCTTTGACCACCTCTTGTATACACCGTACTATGTGGCTCCAGA 686

Db 1476 CTTTCGCCCCAGGTCAAGTATTCACTGATGTTGTTGGTAGCCCTTACTATGTGCGGCCAGA 1535

QY 687 AGTGCTGGGTCCAGAGAAAGTATGACAAGTCTCTGTGACATGTGGTCCCTGGGTGTCATCAT 746

Db 1536 AGTTCTGAA--AAAGAAATATGGTCAAGAGGCAGATGTCTGGAGCGCTGGTGTGATAAT 1592

QY 747 GTACATCCTGCTGTGTGGGTATCCCCCCTTCTTACTCCAAACACGCGCCTTGCCATCTCTCC 806

Db 1593 TTACATCTTGTGTGTGGTGTGCCGCCATTTTGGGCAGAGAAACGACAGGGTATATTTGA 1652

QY 807 GGGCATGAAGACTCGCATCCGAATGGGCCAGTATGAATTTCCCAACCCAGAATGGTCAGA 866

Db 1653 AGAGGTTTGCATGGTAGAC-----TTGACTTTTCAGTCAGAAACCATGGCCTAG 1700

QY 867 AGTATCAGAGGAAGTGAAGATGCTCATTCGGAATCTGCTGAAAAACAGAGCCCAACCCAGAG 926

Db 1701 CATCTCTGAAGGTGCCAAAGATCTCGTAAGGAGAATGCTTGTTAGGGACCCCGAAGAAGAG 1760

QY 927 AATGACCATCACCGAGTTTATGAACCAACCCCTTGGATCATGCAATCAACAAAGGTCCCTCA 986

Db 1761 ATTGACAGCTCATGAAGTTTTTAAGGCATCCATGGGTCCAGGTTGGTGGTTTGGCTCCTGA 1820

QY 987 AACCCCACTGCA 998

Db 1821 CAAGCCCCCTGGA 1832

RESULT 14

US-11-312-958-35

; Sequence 35, Application US/11312958

; Publication No. US20060100152A1

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals, Inc.

; APPLICANT: Rosenfeld, Julie Beth

; APPLICANT: Silos-Santiago, Inmaculada

; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING

; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,

; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,

; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,

; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR

; TITLE OF INVENTION: 13424 MOLECULES

; FILE REFERENCE: MPI02-027P1RNMNMIM

; CURRENT APPLICATION NUMBER: US/11/312,958

; CURRENT FILING DATE: 2005-12-20

; PRIOR APPLICATION NUMBER: US/10/369,022

; PRIOR FILING DATE: 2003-02-19

; PRIOR APPLICATION NUMBER: US 60/360,495

; PRIOR FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 60/370,121

; PRIOR FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: US 60/373,010

; PRIOR FILING DATE: 2002-04-16

; PRIOR APPLICATION NUMBER: US 60/373,908

; PRIOR FILING DATE: 2002-04-19

; PRIOR APPLICATION NUMBER: US 60/377,717

; PRIOR FILING DATE: 2002-05-03

; PRIOR APPLICATION NUMBER: US 60/379,949

; PRIOR FILING DATE: 2002-05-13

; PRIOR APPLICATION NUMBER: US 60/382,409

; PRIOR FILING DATE: 2002-05-21

; PRIOR APPLICATION NUMBER: US 60/385,280

; PRIOR FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: US 60/386,879

; PRIOR FILING DATE: 2002-06-06

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 35

; LENGTH: 2421

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (91)...(2058)

US-11-312-958-35

Query Match 6.7%; Score 79.8; DB 7; Length 2421;

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Best Local Similarity 47.9%; Pred. No. 5.7e-08;
Matches 401; Conservative 0; Mismatches 412; Indels 24; Gaps 5;

QY 133 AAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAGGTCACCGCCAG 192
Db 1132 AAGCCACGGCCCATGGGCATCATTTGCCGCCAATGTGGAAAAGCATTTATGAGACTGGCCGG 1191

QY 193 GTCCTGGGGCTGGGCATCAACGGCAAAGTTTTCAGATCTTCAACAAGAGGACCCAGGAG 252
Db 1192 GTCATTGGGGATGGGAACCTTTGCTGTCGTGAAGGAGTCAGACACCGCAGACCCAGGCAG 1251

QY 253 AAATTGCGCCCTCAAAATGCTTCAGGACTGCCCCCAAGGCCCGCAGGAGGTGGAGCTGCAC 312
Db 1252 GCCTATGCGATGAAGATCATTTGACAAAGTCCAGACTCAAGGGCAAGGAGACATGGTGGAC 1311

QY 313 TGGCGGGCCTCCAGTGTCCCGCACATCGTACGGATCGTGGATGTGTACGAGAAT---CTG 369
Db 1312 AGTGAGATCTTGATCATCCAGAGCCCTCTCTCACCCCAACATCGTGAATTCATGAAGTC 1371

QY 370 TACGCAGGGAGGAAGTGCCTGCTGATTGTCATGGAATGTTTGGACGGTGGAGAACTCTTT 429
Db 1372 TACGAAACAGACATGGAATCTACCTGATCCTGGAGTACGTGCAGGAGGAGACCTTTT 1431

QY 430 AGCCGAATCCAGGATCGAGGAGACCAGGCATTCACAGAAAGAGAGCATCCGAAATCATG 489
Db 1432 GACGCCATCATAGAAAGTG-----TGAAGTCCCGGAGCCCGATGCTGCCCTCATGATC 1485

QY 490 AAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAACATGTCGCCATCGGGATGTC 549
Db 1486 ATGGACTTATGCAAGCCCTCGTCCACATGCACGACAGAGCATTTGTCCACCGGACCTC 1545

QY 550 AAGCCTGAGAAATCTCTTATACACCTCCAAAAGGCCCAA---CGCCATCTGAAACTCACT 606
Db 1546 AAGCCGGAACAACTTTTGGTTCAGCGAAATGAGGACAAATCTACTACCTTGAAATGGCT 1605

QY 607 GACTTTGGCTTTGCCAAGGAAACCCAGCCACAACTCTTTGACCACCTCTTGTATATACA 666
Db 1606 GATTTTGGACTTGCAAGCATGTGTGAGAC-----CTATATTACTGTGTGGGACC 1659

QY 667 CCGTACTATGTGGCTCCAGAAGTGTGGTCCAGAGAAGTATGACAAGTCCCTGTGACATG 726
Db 1660 CCAACTTACGTAGCTCCCGAAATCTTCTGAGAAAGGTTATGGAAGTGGAGTGGACATG 1719

QY 727 TGGTCCCTGGGTGTCATCATGTACATCCTGCTGTGTGGGTATCCCCCTTCTACTCCAAC 786
Db 1720 TGGGTGCTGGCGTGATCCTCTATATCCTGCTGTGTGGCTTTCCCCCATTCGCGAGCCCT 1779

QY 787 CACGGCCTTGCCATCTCTCCGGCATGAAGACTCGCATCCGAATGGGCCAGTATGAATTT 846
Db 1780 GAGAGGACCCAGGACGAGCTCTTTAACA-----TCATCCAGTGGGCCACTTTGAGTTC 1833

QY 847 CCAACCCAGAAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAATCTGCTG 906
Db 1834 CTCGCCCTTACTGGGACAAATATCTCTGATGCTGTCTAAGATCTGGTGAGCCGTTGCTG 1893

QY 907 AAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGGATC 963
Db 1894 GTGGTAGACCCCAAAAAGCGCTACACAGCTCATCAGGTTCTTCAGCACCCCTGGATC 1950

RESULT 15
US-11-312-958-3
; Sequence 3, Application US/11312958
; Publication No. US20060100152A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1675, 9569 OR
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; TITLE OF INVENTION: 13424 MOLECULES
; FILE REFERENCE: MPI02-027P1RNMNIM
; CURRENT APPLICATION NUMBER: US/11/312,958
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/10/369,022
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/360,495
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/370,121
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/373,010
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/373,908
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/377,717
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/379,949
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/382,409
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/385,280
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/386,879
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4726
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)...(1828)
US-11-312-958-3

Query Match 6.7%; Score 79.8; DB 7; Length 4726;
Best Local Similarity 47.9%; Pred. No. 6.6e-08;
Matches 401; Conservative 0; Mismatches 412; Indels 24; Gaps 5;

QY 133 AAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAGGTCACCGCCAG 192
Db 902 AAGCCACGGCCCATGGGCATCATTTGCCCCAATGTGGAAAAGCATTTATGAGACTGGCCGG 961

QY 193 GTCCTGGGGCTGGGCATCAACGGCAAAGTTTTCAGATCTTCAACAAGAGGACCCAGGAG 252
Db 962 GTCATTGGGGATGGGAACCTTGTCTGCTGAAGGAGTGCAGACACCCGAGACCCAGGCAG 1021

QY 253 AAATTGCGCCCTCAAAATGCTTCAGGACTGCCCCCAAGGCCCGCAGGAGGTGGAGCTGCAC 312
Db 1022 GCCTATGCGATGAAGATCATTTGACAAAGTCCAGACTCAAGGGCAAGGAGACATGGTGGAC 1081

QY 313 TGGCGGGCCTCCAGTGTCCCGCACATCGTACGGATCGTGGATGTGTACGAGAAT---CTG 369
Db 1082 AGTGAGATCTTGATCATCCAGAGCCCTCTCTCACCCCAACATCGTGAATTCATGAAGTC 1141

QY 370 TACGCAGGGAGGAAGTGCCTGCTGATTGTTCATGGAATGTTTGGACGGTGGAGAACTCTTT 429
Db 1142 TACGAAACAGACATGGAATCTACTGATCTCTGGAGTACGTGCAGGGAGGAGACCTTTT 1201

QY 430 AGCCGAATCCAGGATCGAGGAGACCCAGGCATTCACAGAAAAGAGAGCATCCGAAATCATG 489
Db 1202 GACGCCATCATAGAAAGTG-----TGAAGTTCCCGGAGCCCGATGCTGCCCTCATGATC 1255

QY 490 AAGAGCATCGGTGAGGCCATCCAGTATCTGCAATTCATCAATCAACATTTGCCCATCGGGATGTC 549
Db 1256 ATGGACTTATGCAAGCCCTCGTCCACATGCACGACAGAGCATTTGTCCACCGGACCTC 1315

QY 550 AAGCCTGAGAAATCTCTTATACACCTCCAAAAGGCCCAA---CGCCATCTCTGAAACTCACT 606
Db 1316 AAGCCGGAACAACTTTTGGTTCAGCGAAATGAGGACAAATCTACTACCTTGAATTTGGCT 1375

QY 607 GACTTTGGCTTTGCCAAGGAAACCCAGCCACAACTCTTTTGACCACCTCTTGTATATACA 666
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Db

1376

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1429

QY

667

CCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAAGTATGACAAGTCCTGTGACATG

726

Db

1430

CCAACTTACGTAGTCCCGAAATTCTTCTGAGAAAGTTATGGACTGGAGGTGGACATG

1489

QY

727

TGGTCCCTGGGTGTCATCATGTACATCCTGTCTGTGGGTATCCCCCCTTCTACTCCAAC

786

Db

1490

TGGGCTGCTGGCGTGATCCTCTATATCCTGTGTGTGGCTTTCCCCCATTCGCGAGCCCT

1549

QY

787

CACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTATGAATTT

846

Db

1550

GAGAGGGACCCAGGACGAGCTCTTTAACA-----TCATCCAGCTGGGCCACTTTGAGTTC

1603

QY

847

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906

Db

1604

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1663

QY

907

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963

Db

1664

GTGGTAGACCCCAAAAAGCGGTACACAGCTCATCAGGTTCTTCAGCACCCCTGGATC

1720

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2006, 15:49:29 ; Search time 848 Seconds
(without alignments)
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Perfect score: 1191
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Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
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- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1191	100.0	1203	8	Aad50037 Human ful
3	1186.2	99.6	1203	14	Adv43403 Human psy
4	1186.2	99.6	1726	12	Adm36339 Human MK2
5	1186.2	99.6	1726	14	Adx06659 Cyclin-de
6	1181.4	99.2	1336	6	Abk84657 Human cDN
7	1181.4	99.2	1336	11	Adi32071 Human cDN
8	1181.4	99.2	1336	13	Ads84138 Human lym
9	1080.2	90.7	2802	3	Aaf15803 Human pro
10	1050.4	88.2	2592	13	Acn41322 Human dia
11	1048.4	88.0	1113	14	Adv43402 Human psy
12	1048.4	88.0	1128	12	Adp87584 Human NOV
13	1048.4	88.0	2258	6	AbL67227 Thyroid c
14	1048.4	88.0	2258	10	ACA56817 Human sig
15	1048.4	88.0	2258	12	ADI56613 Human pol
16	1048.4	88.0	2258	12	ADP87578 Human NOV
17	1048.4	88.0	2258	14	AED17914 Fibrotic
18	1048.4	88.0	2263	6	ABV73995 Human MAP

19	1048.4	88.0	2263	9	ACA62272	Aca62272 Human DNA
20	1048.4	88.0	2263	12	ADM36337	Adm36337 Human MK2
21	1048.4	88.0	2263	14	ADX06657	Adx06657 Cyclin-de
22	1048.4	88.0	2263	14	ADY86797	Ady86797 Human MAP
23	1048.4	88.0	2263	14	AEA89439	Aea89439 Human MAP
24	1048.4	88.0	3608	14	ADZ49304	Adz49304 Insulin s
25	1038.8	87.2	1130	12	ADP87582	Adp87582 Human NOV
26	1038.8	87.2	1133	12	ADP87586	Adp87586 Human NOV
27	1002.4	84.2	1026	12	ADP87588	Adp87588 Human NOV
28	982	82.5	1305	9	ACF57389	Acf57389 SUMO-MPAK
29	972	81.6	981	12	ADN61587	Adn61587 DNA encod
30	904.4	75.9	3186	8	ACC46238	Acc46238 Human dit
31	876.8	73.6	885	12	ADP87580	Adp87580 Human NOV
32	876.8	73.6	885	12	ADP87590	Adp87590 Human NOV
33	836.4	70.2	1168	14	AEEL13869	Aeel13869 Hamster c
34	591.4	49.7	690	12	ADP87652	Adp87652 Rat MAPKA
35	562	47.2	614	14	ACL61582	Acl61582 Human col
36	555.8	46.7	1149	14	AEEL19658	Aeel19658 Human MAP
37	555.8	46.7	1298	6	ABK84332	Abk84332 Human cDN
38	555.8	46.7	2481	6	ABK84214	Abk84214 Human cDN
39	555.8	46.7	2481	6	ABK13301	Abk13301 DNA encod
40	555.8	46.7	2481	10	ADD14766	Add14766 Human src
41	555.8	46.7	2481	10	ACA56490	Aca56490 Human sig
42	555.8	46.7	2481	12	ADI56286	Adi56286 Human pol
43	555.8	46.7	2481	12	ADO52389	Ado52389 Human BRC
44	555.8	46.7	2500	12	ADP21372	Adp21372 Gene MAPK
45	555.8	46.7	2500	12	ADQ87216	Adq87216 Human tum

ALIGNMENTS

RESULT 1
AAD50036
ID AAD50036 standard; cDNA; 1191 BP.
XX
AC AAD50036;
XX
DT 24-MAR-2003 (first entry)
XX
DE Human truncated MAPKAP-2 kinase, tdnMAPKAP-2 cDNA.
XX
KW Human; mitogen-activated protein kinase activating protein kinase-2;
KW MAPKAP-2 kinase; signal transduction; cell proliferative disorder;
KW immune system disorder; inflammation; arthritis; immunomodulator;
KW cytostatic; gene therapy; enzyme; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1191
FT /*tag= a
FT /product= "Human tdnMAPKAP-2"
FT /note= "No start codon"
FT /partial

XX WO200290524-A2.
PN
XX
XX
PD 14-NOV-2002.
XX
PF 25-FEB-2002; 2002WO-US005670.
XX
PR 28-FEB-2001; 2001US-0272260P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Lograsso P, Hawkins J, Lisnock JM;
XX
DR WPI; 2003-111970/10.
DR P-PSDB; AAE29898.

XX
PT New isolated nucleic acid molecule encoding a human mitogen-activated protein kinase activating protein kinase-2 (MAPKAP-2), useful for

PT treating immune-system related disorders, inflammation and arthritis.
XX Claim 1; Fig 1; 150pp; English.
PS The invention relates to an isolated nucleic acid molecule comprising a
XX sequence of nucleotides that encode a human mitogen-activated protein
CC kinase activating protein kinase-2 (MAPKAP-2 kinase) and a coding region
CC that encodes a splice variant of a MAPKAP-2 kinase. The invention is
CC especially useful in regulating signal transduction in a cell and in
CC diagnosing or treating MAPKAP-2-mediated disorders eg. cell proliferative
CC disorders, immune system disorders, inflammation, arthritis. The nucleic
CC acid and the polypeptide may also be used in screening assays, predictive
CC medicine, diagnostic or prognostic assays, chromosome mapping, tissue
CC typing, pharmacogenomics and in monitoring clinical trials. The invention
CC is useful in gene therapy. The present sequence is human truncated MAPKAP
CC -2 kinase, tdnaMAPKAP-2 cdna
XX
SQ Sequence 1191 BP; 300 A; 362 C; 311 G; 218 T; 0 U; 0 Other;

Query Match 100.0%; Score 1191; DB 8; Length 1191;
Best Local Similarity 100.0%; Pred. No. 1.7e-260;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCCCGCCCCCGCGCCGAGCCCCC 60
DB 1 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCCCGCCCCCGCGCCGAGCCCCC 60

QY 61 ACCCTGTCCTGCCGACCCCCCGCGGAGCGCGCCCGCCCCCGCGCAGATTCCCG 120
DB 61 ACCCTGTCCTGCCGACCCCCCGCGGAGCGCGCCCGCCCCCGCGCAGATTCCCG 120

QY 121 CAGTTCACGTCAAGTCCGGCCTGCAGATCAAGAAGAAGCGCCATCATCGACTACAAG 180
DB 121 CAGTTCACGTCAAGTCCGGCCTGCAGATCAAGAAGAAGCGCCATCATCGACTACAAG 180

QY 181 GTCACAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAAAGTTTGCAGATCTTCAACAAG 240
DB 181 GTCACAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAAAGTTTGCAGATCTTCAACAAG 240

QY 241 AGGACCCAGGAGAAATTGCGCCTCAAAATGCTTCAGGACTGCCCCAGGCCCGCAGGGAG 300
DB 241 AGGACCCAGGAGAAATTGCGCCTCAAAATGCTTCAGGACTGCCCCAGGCCCGCAGGGAG 300

QY 301 GTGGAGCTGCACCTGCGCGGCCCTCCCAGTGCCTCCGCACATCGTACGGATCTGTGGATGTATC 360
DB 301 GTGGAGCTGCACCTGCGCGGCCCTCCCAGTGCCTCCGCACATCGTACGGATCTGTGGATGTATC 360

QY 361 GAGAAATCTGTACGAGGGAGGAAGTGCTGTGATTTGCATGGAATGTTGGACGGTGA 420
DB 361 GAGAAATCTGTACGAGGGAGGAAGTGCTGTGATTTGCATGGAATGTTGGACGGTGA 420

QY 421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACGAGCATTCACAGAAGAGAGCATCC 480
DB 421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACGAGCATTCACAGAAGAGAGCATCC 480

QY 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAATCAACATTGCCCAT 540
DB 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAATCAACATTGCCCAT 540

QY 541 CGGGATGTCAAGCCTGAGAAATCTCTTATACCTCCAAAAGGCCCAACGCCATCCTGAAA 600
DB 541 CGGGATGTCAAGCCTGAGAAATCTCTTATACCTCCAAAAGGCCCAACGCCATCCTGAAA 600

QY 601 CTCACCTGACTTTGGCTTTGCCAAGGAAACCACGAGCCACAACCTCTTTGACCACTCCTTGT 660
DB 601 CTCACCTGACTTTGGCTTTGCCAAGGAAACCACGAGCCACAACCTCTTTGACCACTCCTTGT 660

QY 661 TATACACCGTACTATGTGGCTCCAGAAGTCTGGTCCAGAGAAGTATGACAAGTCTTGT 720
DB 661 TATACACCGTACTATGTGGCTCCAGAAGTCTGGTCCAGAGAAGTATGACAAGTCTTGT 720

QY 721 GACATGTGGTCCCTGGTGTTCATGTACATCTCTGTGTGGGTATCCCCCTTCTAC 780
DB 721 GACATGTGGTCCCTGGTGTTCATGTACATCTCTGTGTGGGTATCCCCCTTCTAC 780

Db 721 GACATGTGGTCCCTGGTGTTCATGTACATCCTGCTGTGGGTATCCCCCTTCTAC 780
QY 781 TCCAAACACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
DB 781 TCCAAACACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
QY 841 GAATTTCCCAACCCAGAAATGGTCAGAAATATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
DB 841 GAATTTCCCAACCCAGAAATGGTCAGAAATATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
QY 901 CTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 960
DB 901 CTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 960
QY 961 ATCATGCAATCAACAAAGGTCCTCAAAACCCCACTGCACACCAAGCGGTCCTGAAGGAG 1020
DB 961 ATCATGCAATCAACAAAGGTCCTCAAAACCCCACTGCACACCAAGCGGTCCTGAAGGAG 1020
QY 1021 GACAAGAGCGGTGGAGGATGTCAAGGAGGAGATGACCATGTCCTTGGCCACAATGCGC 1080
DB 1021 GACAAGAGCGGTGGAGGATGTCAAGGAGGAGATGACCATGTCCTTGGCCACAATGCGC 1080
QY 1081 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGATCAACCCCTCTGTGCTGTG 1140
DB 1081 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGATCAACCCCTCTGTGCTGTG 1140
QY 1141 AAGAGCGGAAAGAAAGCTCGGGCCTGGAGGCTGCGGCTCTGGCCCACTGA 1191
DB 1141 AAGAGCGGAAAGAAAGCTCGGGCCTGGAGGCTGCGGCTCTGGCCCACTGA 1191

RESULT 2
AAD50037
ID AAD50037 standard; cdna; 1203 BP.
XX
AC AAD50037;
XX 24-MAR-2003 (first entry)
XX Human full length MAPKAP-2 kinase, fldnaMAPKAP-2 cDNA.
DE Human; mitogen-activated protein kinase activating protein kinase-2;
KW MAPKAP-2 kinase; signal transduction; cell proliferative disorder;
KW immune system disorder; inflammation; arthritis; immunomodulator;
KW cytosstatic; gene therapy; enzyme; gene; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 1..1203
FT /*tag= a
FT /product= "Human fldnaMAPKAP-2"
XX WO200290524-A2.
XX 14-NOV-2002.
XX 25-FEB-2002; 2002WO-US005670.
XX 28-FEB-2001; 2001US-0272260P.
XX (MERI) MERCK & CO INC.
PI Lograsso P, Hawkins J, Lisnock JM;
XX WPI; 2003-111970/10.
DR P-PSDB; AAE29899.
XX New isolated nucleic acid molecule encoding a human mitogen-activated
PT protein kinase activating protein kinase-2 (MAPKAP-2), useful for
PT treating immune-system related disorders, inflammation and arthritis.
XX Claim 63; Fig 3; 150pp; English.
PS

XX The invention relates to an isolated nucleic acid molecule comprising a
CC sequence of nucleotides that encode a human mitogen-activated protein
CC kinase activating protein kinase-2 (MAPKAP-2 kinase) and a coding region
CC that encodes a splice variant of a MAPKAP-2 kinase. The invention is
CC especially useful in regulating signal transduction in a cell and in
CC diagnosing or treating MAPKAP-2-mediated disorders eg. cell proliferative
CC disorders, immune system disorders, inflammation, arthritis. The nucleic
CC acid and the polypeptide may also be used in screening assays, predictive
CC medicine, diagnostic or prognostic assays, chromosome mapping, tissue
CC typing, pharmacogenomics and in monitoring clinical trials. The invention
CC is useful in gene therapy. The present sequence is human full length
CC MAPKAP-2 kinase, fldnaMAPKAP-2 cDNA
XX

SQ Sequence 1203 BP; 303 A; 366 C; 313 G; 221 T; 0 U; 0 Other;

Query Match 100.0%; Score 1191; DB 8; Length 1203;
Best Local Similarity 100.0%; Pred. No. 1.7e-260;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCAGGGCCAGAGCCCGCGTGCCTTCCCGCCCCCGCCCCCGCGCAGCCCCC 60
DB 13 TCCAGGGCCAGAGCCCGCGTGCCTTCCCGCCCCCGCCCCCGCGCAGCCCCC 72
QY 61 ACCCTGCCCTGCCGACCCCCCGCGCAGCGCGCGCCCCCGCCCCCGCGCAGTTCCCG 120
DB 73 ACCCTGCCCTGCCGACCCCCCGCGCAGCGCGCGCCCCCGCCCCCGCGCAGTTCCCG 132
QY 121 CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGACTACAAG 180
DB 133 CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGACTACAAG 192
QY 181 GTCACCAGCCAGTCTCTGGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAG 240
DB 193 GTCACCAGCCAGTCTCTGGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAG 252
QY 241 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCAAAGCCCGCAGGGAG 300
DB 253 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCAAAGCCCGCAGGGAG 312
QY 301 GTGGAGCTGCACTGGCGGGCCTCCAGTGCOCGCACATCGTACGGATCGTGGATGTGTAC 360
DB 313 GTGGAGCTGCACTGGCGGGCCTCCAGTGCOCGCACATCGTACGGATCGTGGATGTGTAC 372
QY 361 GAGAACTGTACGAGGGAGGAAGTGCCCTGCTGATGTGATGGAATGTTGGACGGTGA 420
DB 373 GAGAACTGTACGAGGGAGGAAGTGCCCTGCTGATGTGATGGAATGTTGGACGGTGA 432
QY 421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGAGCATCC 480
DB 433 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGAGCATCC 492
QY 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 540
DB 493 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 552
QY 541 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCCATCCTGAAA 600
DB 553 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCCATCCTGAAA 612
QY 601 CTCACGTACTTTGGCTTTGCCAAGGAAACACACAGCCACAACTCTTTGACCACTCCTTGT 660
DB 613 CTCACGTACTTTGGCTTTGCCAAGGAAACACACAGCCACAACTCTTTGACCACTCCTTGT 672
QY 661 TATACACCGTACTATGTGGTCCAGAAAGTGGTCCAGAGAGATGACAAGTCCCTGT 720
DB 673 TATACACCGTACTATGTGGTCCAGAAAGTGGTCCAGAGAGATGACAAGTCCCTGT 732
QY 721 GACATGTGGTCCCTGGGTGTCATCATGTACATCCTGCTGTGGGTATCCCCCTTCTAC 780
DB 733 GACATGTGGTCCCTGGGTGTCATCATGTACATCCTGCTGTGGGTATCCCCCTTCTAC 792
QY 781 TCCAAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840

DB 793 TCCAAACCACGGCCTTGCCATCTCTCCGGCATGAAGACTCGCATCCGAATGGCCAGTAT 852
QY 841 GAATTTCCCAACCCAGAAATGGTCAGAACTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
DB 853 GAATTTCCCAACCCAGAAATGGTCAGAACTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 912
QY 901 CTGCTGAAACAGAGCCACCAGAGAAATGACCATCACCCAGCGGCTCTGAAGGAG 960
DB 913 CTGCTGAAACAGAGCCACCAGAGAAATGACCATCACCCAGCGGCTCTGAAGGAG 972
QY 961 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCAGCCGGTCTGAAGGAG 1020
DB 973 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCAGCCGGTCTGAAGGAG 1032
QY 1021 GACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTGGCCACAATGCCG 1080
DB 1033 GACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTGGCCACAATGCCG 1092
QY 1081 GTTGACTACGAGCAGATCAAGATAAAAGATTGAAGATGCATCCAAACCTCTGCTGCTG 1140
DB 1093 GTTGACTACGAGCAGATCAAGATAAAAGATTGAAGATGCATCCAAACCTCTGCTGCTG 1152
QY 1141 AAGAGGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCACTGA 1191
DB 1153 AAGAGGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCACTGA 1203

RESULT 3
ADV43403

ID ADV43403 standard; cDNA; 1203 BP.

XX AC ADV43403;

XX DT 10-MAR-2005 (first entry)

XX DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1031.

XX KW microarray; psychoneuroendocrinimmune; chronic fatigue;

XX KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;

XX KW cancer; neoplasm; infection; expressed sequence tag; ss.

XX OS Homo sapiens.

XX PN WO2004108899-A2.

XX PD 16-DEC-2004.

XX PF 04-JUN-2004; 2004WO-US017686.

XX PR 04-JUN-2003; 2003US-0475915P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Nicholson A, Vernon SD;

XX PS WPI; 2005-031682/03.

XX PT New microarray comprising probes for genes involved in

XX PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a

XX PT condition associated with PNI activity, e.g., inflammatory or infectious

XX PS Claim 1; SEQ ID NO 1031; 254pp; English.

XX CC The invention relates to a new microarray which comprises probes for

XX CC genes involved in psychoneuroendocrinimmune (PNI) activity. The

XX CC microarray is useful in diagnosing a condition associated with PNI

XX CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,

XX CC cancer and infection. The present sequence represents a

XX CC psychoneuroendocrinimmune gene expressed sequence tag. Note the

XX CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to

CC SEQ ID NO 1829 are provided.

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XX
SQ      Sequence 1203 BP; 303 A; 365 C; 313 G; 222 T; 0 U; 0 Other;

      Query Match      99.6%; Score 1186.2; DB 14; Length 1203;
      Best Local Similarity 99.7%; Pred. No. 2.1e-259;
      Matches 1188; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1   TCCCAGGGCCAGAGCCGCGCGGTGCCGTTCCCGCCGCGCGGCCCGCCCGCGCAGCGCCCGCC 60
Db      13   TCCCAGGGCCAGAGCCGCGCGGTGCCGTTCCCGCGCGCGGCCCGCCCGCGCAGCGCCCGCC 72

QY      61   ACCCCTGCCCTGCCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db      73   ACCCCTGCCCTGCCGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 132

QY      121  CAGTTCACGTCAAAGTCGGCCTGCAGATCAAGAAGAAGCCCATCATCGATGACTACAAG 180
Db      133  CAGTTCACGTCAAAGTCGGCCTGCAGATCAAGAAGAAGCCCATCATCGATGACTACAAG 192

QY      181  GTCACACGCGAGGTCTTGGGGCTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG 240
Db      193  GTCACACGCGAGGTCTTGGGGCTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG 252

QY      241  AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCCAAGGCCCGCAGGGAG 300
Db      253  AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCCAAGGCCCGCAGGGAG 312

QY      301  GTGGAGCTGCACTGGCGGCCTCCAGTGCCCGCAGCATCGTACGGATCGTGGATGTGTAC 360
Db      313  GTGGAGCTGCACTGGCGGCCTCCAGTGCCCGCAGCATCGTACGGATCGTGGATGTGTAC 372

QY      361  GAGAAATCTGTACGACGAGGAGAAAGTGCCCTGCTGATTTGTTCATGGAATGTTTGGACGGTGA 420
Db      373  GAGAAATCTGTACGACGAGGAGAAAGTGCCCTGCTGATTTGTTCATGGAATGTTTGGACGGTGA 432

QY      421  GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCCAGGCATTCACAGAAAGAGAGCATCC 480
Db      433  GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCCAGGCATTCACAGAAAGAGAGCATCC 492

QY      481  GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTTCAATCAACATTCGCCCAT 540
Db      493  GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTTCAATCAACATTCGCCCAT 552

QY      541  CGGGATGTCAAGCCTGAGAATCTTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 600
Db      553  CGGGATGTCAAGCCTGAGAATCTTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 612

QY      601  CTCACGTGACTTTGGCTTTGCCAAGGAAACCCAGGCACCAAACTCTTTGACCACTCCTTGT 660
Db      613  CTCACGTGACTTTGGCTTTGCCAAGGAAACCCAGGCACCAAACTCTTTGACCACTCCTTGT 672

QY      661  TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCCTGT 720
Db      673  TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCCTGT 732

QY      721  GACATGTGGTCCCTGGGTGTCATCATGTACATCCCTGTGTGGGTATCCCCCCTTCTAC 780
Db      733  GACATGTGGTCCCTGGGTGTCATCATGTACATTTCTGTGTGGGTATCCCCCCTTCTAC 792

QY      781  TCCAAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
Db      793  TCCAAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 852

QY      841  GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
Db      853  GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 912

QY      901  CTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 960
Db      913  CTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 972

QY      961  ATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCCAGCCGGGTCTCTGAAGGAG 1020

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CC MK2 modulator. The compound has vasotropic, cerebroprotective, cardiant, CC hypotensive, antiarteriosclerotic, thrombolytic, neuroprotective, CC cardiovascular, antianginal and antiarrhythmic activities, and can be CC used as an MK2 antagonist. The method is useful reducing or treating CC ischaemic injury, particularly cerebral ischaemia. Compounds identified CC by the method are useful for treating ischaemia, (e.g. ischaemia CC resulting from vascular occlusion, cerebral infarction, stroke, and CC related cerebral vascular diseases), myocardial infarction, coronary CC artery disease, congestive heart failure, cardiac arrhythmias, unstable CC angina, high blood pressure, claudication, peripheral occlusive arterial CC disease, atherosclerosis, thrombotic or thromboembolic conditions, or CNS CC disorders associated with cerebral ischaemia. The present sequence CC encodes the human MK2 variant 2, which is located on chromosome 1q32. CC XX

SEQ Sequence 1726 BP; 411 A; 543 C; 481 G; 291 T; 0 U; 0 Other;

Query Match 99.6%; Score 1186.2; DB 12; Length 1726;
Best Local Similarity 99.7%; Pred. No. 2.3e-259;
Matches 1188; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCGCCCGCCCGCGCGAGCCCCC 60
Db 391 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCGCCCGCCCGCGCGAGCCCCC 450
QY 61 ACCCCTGCCCTGCCGACCCCCCGCGCAGCCGCGCCCGCCCGCCCGCAGATTCCCG 120
Db 451 ACCCCTGCCCTGCCGACCCCCCGCGCAGCCGCGCCCGCCCGCCCGCAGATTCCCG 510
QY 121 CAGTTCACGTC AAGTC CGGCCTGCAGATCAAGAGAACGCCATCATCGATGACTACAAG 180
Db 511 CAGTTCACGTC AAGTC CGGCCTGCAGATCAAGAGAACGCCATCATCGATGACTACAAG 570
QY 181 GTCACCAGCCAGGTCCTGGGGCTGGGCATCAACGCCAAAGTTTTGTCAGATCTTCAACAAG 240
Db 571 GTCACCAGCCAGGTCCTGGGGCTGGGCATCAACGCCAAAGTTTTGTCAGATCTTCAACAAG 630
QY 241 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCAAAGCCCGCAGGGAG 300
Db 631 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCAAAGCCCGCAGGGAG 690
QY 301 GTGGAGCTGC ACTGCGGGCCCTCCAGTGCCCGACATCGTACGGATCGTGGATGTGTAC 360
Db 691 GTGGAGCTGC ACTGCGGGCCCTCCAGTGCCCGACATCGTACGGATCGTGGATGTGTAC 750
QY 361 GAGAATCTGTACG CAGGGAGGAAGTGCCCTGTGATGTGATGTAATGTTGGACGGTGA 420
Db 751 GAGAATCTGTACG CAGGGAGGAAGTGCCCTGTGATGTGATGTAATGTTGGACGGTGA 810
QY 421 GAACTCTTTAGCC GAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGAGCATCC 480
Db 811 GAACTCTTTAGCC GAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGAGCATCC 870
QY 481 GAAATCATGAAGC ATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 540
Db 871 GAAATCATGAAGC ATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 930
QY 541 CGGGATGTCAAGC CTGAGAAATCTTTATACACTTCCAAAAGGCCCAACGCCATCCTGAAA 600
Db 931 CGGGATGTCAAGC CTGAGAAATCTTTATACACTTCCAAAAGGCCCAACGCCATCCTGAAA 990
QY 601 CTCACTGACTTTG GCTTTGCCAAGGAAACCACAGCCACAACTCTTTGACCACCTCTTGT 660
Db 991 CTCACTGACTTTG GCTTTGCCAAGGAAACCACAGCCACAACTCTTTGACCACCTCTTGT 1050
QY 661 TATACACCGTACT ATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCCTGT 720
Db 1051 TATACACCGTACT ATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCCTGT 1110
QY 721 GACATGTGGTCCC TGCGGTGTCATCATGTACATCTCTGTGTGTGGGTATCCCCCTTCTAC 780
Db 1111 GACATGTGGTCCC TGCGGTGTCATCATGTACATCTCTGTGTGTGGGTATCCCCCTTCTAC 1170
QY 781 TCCAAACCACGGC CTTGCCATCTCTCCGGGCAATGAAGACTCGCATCCGAATGGGCCAGTAT 840

Db 1171 TCCAAACCACGGCCTTGCCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
QY 841 GAATTTCCCAACCCAGAAATGGTCAGAAATGTCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
Db 1231 GAATTTCCCAACCCAGAAATGGTCAGAAATGTCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
QY 901 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGG 960
Db 1291 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGG 1350
QY 961 ATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCAAGCCGGGTCTGAAAGGAG 1020
Db 1351 ATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCAAGCCGGGTCTGAAAGGAG 1410
QY 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCATGCGTGCCTTGGCCACAATGCGC 1080
Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCATGCGTGCCTTGGCCACAATGCGC 1470
QY 1081 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCACCCCTCTGCTGCTG 1140
Db 1471 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCACCCCTCTGCTGCTG 1530
QY 1141 AAGAGCGGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCACTGA 1191
Db 1531 AAGAGCGGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCACTGA 1581

RESULT 5

ADX06659
ID ADX06659 standard; DNA; 1726 BP.
XX
AC ADX06659;
XX
DT 21-APR-2005 (first entry)
XX
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 1224.
XX
KW cytostatic; cyclin-dependent kinase; cdk; biomarker; gene; ds.
XX
OS Homo sapiens.
XX
PN W02005012875-A2.
XX
PD 10-FEB-2005.
XX
PF 29-JUL-2004; 2004WO-US024424.
XX
PR 29-JUL-2003; 2003US-0490890P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX
XX WPI; 2005-163068/17.
DR P-PSDB; ADX06650.
XX
PT Biomarkers useful for predicting or determining the response of a mammal
PT to a cancer treatment comprising administration of a modulator of cyclin-
PT dependent kinase activity.
XX
PS Claim 5; SEQ ID NO 1224; 141pp; English.
XX

CC This invention describes a novel method of predicting or determining
CC whether a mammal will respond or is responding to an anti-cancer agent
CC that modulates cyclin-dependent kinase (cdk) activity. The method
CC comprises measuring the level of one or more biomarkers selected from
CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
CC invention is utilized in a kit for determining or predicting whether
CC patient would be susceptible or resistant to treatment by an agent
CC modulating cdk activity. The invention also describes a method for
CC utilizing individualized genetic profiles for treating diseases and

CC disorders based on patient's response and molecular level, specialized
CC microarrays comprising the biomarkers described, antibodies directed
CC against the biomarkers and a cell culture model to identify biomarkers.
CC The cdk modulator is preferably N-5-[(5-(1,1-Dimethylethyl)-2-
CC oxazolyl)methyl]thiol-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
CC tartaric acid salt. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct sequences. This
CC sequence encodes a biomarker used in the method of the invention.
XX
SQ Sequence 1726 BP; 411 A; 543 C; 481 G; 291 T; 0 U; 0 Other;

Query Match 99.6%; Score 1186.2; DB 14; Length 1726;
Best Local Similarity 99.7%; Pred. No. 2.3e-259;
Matches 1188; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCCCGCCCCCGCGCGCAGCCCCC 60
Db 391 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCCCGCCCCCGCGCGCAGCCCCC 450

QY 61 ACCCCTGCCCTGCCGACCCCCCGCGCAGCCGCGCCGCCGCCGCCCGCAGTTCCCG 120
Db 451 ACCCCTGCCCTGCCGACCCCCCGCGCAGCCGCGCCGCCGCCGCCCGCAGTTCCCG 510

QY 121 CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATACAAG 180
Db 511 CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATACAAG 570

QY 181 GTCACCAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTTTGAGATCTTCAACAAG 240
Db 571 GTCACCAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTTTGAGATCTTCAACAAG 630

QY 241 AGGACCCAGGAGAAATTCGCCCTCAAAATGTTTCAGGACTGCCCCAGGCCCGCAGGGAG 300
Db 631 AGGACCCAGGAGAAATTCGCCCTCAAAATGTTTCAGGACTGCCCCAGGCCCGCAGGGAG 690

QY 301 GTGGAGCTGCACTGGCGGGCCTCCAGTGC CGGCACATCGTACGGATCGTGGATGTGTAC 360
Db 691 GTGGAGCTGCACTGGCGGGCCTCCAGTGC CGGCACATCGTACGGATCGTGGATGTGTAC 750

QY 361 GAGAACTCTGTACGAGGGAGGAAGTGCCCTGCTGATGTGTATGGAATGTTGGACGGTGA 420
Db 751 GAGAACTCTGTACGAGGGAGGAAGTGCCCTGCTGATGTGTATGGAATGTTGGACGGTGA 810

QY 421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGACATCC 480
Db 811 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGACATCC 870

QY 481 GAAATCATGAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCTCAATCAACATTGCCCAT 540
Db 871 GAAATCATGAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCTCAATCAACATTGCCCAT 930

QY 541 CGGGATGTCAAGCCTGAGAAATCTCTTTATACCTTCAAAAGGCCCAACGCCATCCTGAAA 600
Db 931 CGGGATGTCAAGCCTGAGAAATCTCTTTATACCTTCAAAAGGCCCAACGCCATCCTGAAA 990

QY 601 CTCACTGACTTTGGCTTTGCCAAGGAAACCAACAGCCACAACTCTTTGACCACTCCTTGT 660
Db 991 CTCACTGACTTTGGCTTTGCCAAGGAAACCAACAGCCACAACTCTTTGACCACTCCTTGT 1050

QY 661 TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCCCTGT 720
Db 1051 TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCCCTGT 1110

QY 721 GACATGTGGTCCCTGGGTGTCAATCATGTACATCTCTGTGTGGGTATCCCCCTTCTAC 780
Db 1111 GACATGTGGTCCCTGGGTGTCAATCATGTACATCTCTGTGTGGGTATCCCCCTTCTAC 1170

QY 781 TCCAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
Db 1171 TCCAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230

QY 841 GAATTTCCCAACCCAGAAATGGTCAAGAGTATCAGAGGAAAGTGAAGATGCTCATTCGGAAT 900

Db 1231 GAATTTCCCAACCCAGAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
QY 901 CTGCTGAAAAACAGAGCCCAACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCCTTGG 960
Db 1291 CTGCTGAAAAACAGAGCCCAACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCCTTGG 1350
QY 961 ATCATGCAATCAACAAAGGTCCTCAAAACCCCACTGCACACCAAGCGGGTCTCTGAAGGAG 1020
Db 1351 ATCATGCAATCAACAAAGGTCCTCAAAACCCCACTGCACACCAAGCGGGTCTCTGAAGGAG 1410
QY 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCATGCTTGGCCACAATGCGC 1080
Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCATGCTTGGCCACAATGCGC 1470
QY 1081 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCAACCCCTCTGCTGCTG 1140
Db 1471 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCAACCCCTCTGCTGCTG 1530
QY 1141 AAGAGCGGAAGAAAGCTCGGGCCTCGAGGGCTGCGGCTCTGCCCCACTGA 1191
Db 1531 AAGAGCGGAAGAAAGCTCGGGCCTCGAGGGCTGCGGCTCTGCCCCACTGA 1581

RESULT 6
ABK84657
ID ABK84657 standard; cDNA; 1336 BP.
XX
AC ABK84657;
XX
DT 14-AUG-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #1228.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
PN WO200228999-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US030821.
XX
PR 03-OCT-2000; 2000US-0237189P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR WPI; 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression of
PT genes associated with granulocyte activation, which serves as diagnostic
PT markers that is useful for monitoring disease states and drug toxicity.
XX
PS Claim 1; SEQ ID NO 1228; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing the
CC expression level to an expression level in an unactivated GC, where
CC differential expression of Gs is indicative of GCA. Also included are
CC modulating (M2) GA by contacting GC with an agent that alters the
CC expression of at least one gene in Gs; (2) screening (M3) for an agent
CC capable of modulating GCA or an inflammation (especially chronic) in a

CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease using the gene expression
CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease, by detecting the level of
CC expression in a sample of the tissue of gene(s) from Gs, where the level
CC of expression of the gene is indicative of inflammation; (4) treating
CC (M5) an inflammation (especially chronic) or in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease, by contacting a tissue having inflammation with an
CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
CC is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful
CC for screening an agent capable of modulating GCA preferably in an
CC inflammation in a tissue; M4 is useful for detecting an inflammation
CC (especially chronic) in a tissue, an allergic response in a subject,
CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
CC disease, ulcerative colitis, periodontal disease; also bacterial
CC infection, viral infection, parasitic infection, protozoal infection,
CC fungal infection and M5 is useful for treating one of the above
CC conditions. The present sequence represents a gene differentially
CC expressed in granulocytes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 1336 BP; 338 A; 406 C; 340 G; 252 T; 0 U; 0 Other;

Query Match 99.2%; Score 1181.4; DB 6; Length 1336;
Best Local Similarity 99.5%; Pred. No. 2.7e-258;
Matches 1185; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCCCGCGCCCGCGCAGCCCCC 60
DB 1 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCCCGCGCCCGCGCAGCCCCC 60
QY 61 ACCCTGTCCTGCCGACCCCCCGCGCAGCCGCGCCCGCGCCCGCGCAGTTCCCG 120
DB 61 ACCCTGTCCTGCCGACCCCCCGCGCAGCCGCGCCCGCGCCCGCGCAGTTCCCG 120
QY 121 CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 180
DB 121 CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 180
QY 181 GTCACACGACGAGTCCCTGGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAG 240
DB 181 GTCACACGACGAGTCCCTGGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAG 240
QY 241 AGGACCCAGGAGAAATTCGCCCTCAAAATGTTTCAGGACTGCCCCAGGCCCGCAGGGAG 300
DB 241 AGGACCCAGGAGAAATTCGCCCTCAAAATGTTTCAGGACTGCCCCAGGCCCGCAGGGAG 300
QY 301 GTGGAGCTGACTGGCGGGCCCTCCAGTGCCTCCGACATCGTACGGATCGTGGATGTGTAC 360
DB 301 GTGGAGCTGACTGGCGGGCCCTCCAGTGCCTCCGACATCGTACGGATCGTGGATGTGTAC 360
QY 361 GAGAATCTGTACGAGGAGGAAGTGCCCTGATGTCATGGAATGTTGGACGGTGA 420
DB 361 GAGAATCTGTACGAGGAGGAAGTGCCCTGATGTCATGGAATGTTGGACGGTGA 420
QY 421 GAACTCTTTAGCGGAATCCAGGATCGAGGACACGAGCATTCACAGAAAGAGAGCATCC 480
DB 421 GAACTCTTTAGCGGAATCCAGGATCGAGGACACGAGCATTCACAGAAAGAGAGCATCC 480
QY 481 GAAATCATGAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 540
DB 481 GAAATCATGAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 540
QY 541 CGGGATGTCAGGCCTGAGAAATCTCTTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 600
DB 541 CGGGATGTCAGGCCTGAGAAATCTCTTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 600

QY 601 CTCACGTGACTTGGCTTTGCCAAGGAAACCACAGCCACAACCTCTTTGACCACCTCTTGT 660
DB 601 CTCACGTGACTTGGCTTTGCCAAGGAAACCACAGCCACAACCTCTTTGACCACCTCTTGT 660
QY 661 TATACACCGTACTATGTGGTCCAGAAAGTGTGGTCCAGAGAAAGTATGACAAAGTCTCTGT 720
DB 661 TATACACCGTACTATGTGGTCCAGAAAGTGTGGTCCAGAGAAAGTATGACAAAGTCTCTGT 720
QY 721 GACATGTGTCCCTGGGTGTCTATCATGTACATCTCTGTGTGGGTATCCCCCTTCTAC 780
DB 721 GACATGTGTCCCTGGGTGTCTATCATGTACATCTCTGTGTGGGTATCCCCCTTCTAC 780
QY 781 TCCAACCCAGCGCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
DB 781 TCCAACCCAGCGCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
QY 841 GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGTCTCATTCGGAAT 900
DB 841 GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGTCTCATTCGGAAT 900
QY 901 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 960
DB 901 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 960
QY 961 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCCAGCCGGTCTCTGAAGGAG 1020
DB 961 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCCAGCCGGTCTCTGAAGGAG 1020
QY 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTGGCCACAATGCGC 1080
DB 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTGGCCACAATGCGC 1080
QY 1081 GTTGACTACGAGCAGATCAAGATATAAAGATTTGAAGATGCATCCAAACCTCTGTGCTG 1140
DB 1081 GTTGACTACGAGCAGATCAAGATATAAAGATTTGAAGATGCATCCAAACCTCTGTGCTG 1140
QY 1141 AAGAGCGGGAAGAAAGCTCGGGCCCTGGAGGGCTCGGGCTCTGGCCCACTGA 1191
DB 1141 AAGAGCGGGAAGAAAGCTCGGGCCCTGGAGGGCTCGGGCTCTGGCCCACTGA 1191

RESULT 7

ADI32071
ID ADI32071 standard; cDNA; 1336 BP.
XX AC ADI32071;
XX DT 17-JUN-2004 (first entry)
XX DE Human cDNA #1397.
XX KW Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
KW osteopathic; antiarthritic; antirheumatic; cytostatic.
OS Homo sapiens.
XX PN US6607879-B1.
XX PD 19-AUG-2003.
XX PF 09-FEB-1998; 98US-00023655.
XX PR 09-FEB-1998; 98US-00023655.
XX PA (INCY-) INCYTE CORP.
XX PI Cocks BG, Stuart SG, Seilhamer JJ;
XX DR WPI; 2003-895307/82.

XX A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.

PS Claim 1; SEQ ID NO 1397; 50pp; English.

The invention relates to a composition comprising a plurality of cDNAs for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes, detecting the hybridisation complexes and comparing the levels of the detected hybridisation complexes with the level of hybridisation complexes detected in a non-diseased sample, where an altered level of the detected hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a method for identifying a plurality of polynucleotide probes. The cDNAs are useful as hybridisable array elements in a microarray for monitoring the expression of target polynucleotides. The microarray can be used in the diagnosis of an immunopathology, such as Crohn's disease, asthma, ulcerative colitis, hypereosinophilia, irritable bowel syndrome, osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in identifying agents for the treatment of the diseases. The microarray may also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition may also be used in purification of a subpopulation of mRNAs, cDNAs or genomic fragments. This sequence represents a human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 1336 BP; 338 A; 406 C; 340 G; 252 T; 0 U; 0 Other;

```

Query Match          99.2%; Score 1181.4; DB 11; Length 1336;
Best Local Similarity 99.5%; Pred. No. 2.7e-258;
Matches 1185; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

Qy		1	TCCCAGGGCCAGAGCCCCCGGTGCGTTCCTCCCGGCCCGGCCCGCCCGCGCAGAGCCCCCCC	60
Db		1	TCCCAGGGCCAGAGCCCCCGGTGCGTTCCTCCCGGCCCGGCCCGCCCGCGCAGAGCCCCCCC	60
Qy		61	ACCCCTGCCTGCCGCAACCCCGGGCAGCCCGCGCGCGCCCGCCCGCGCAGCAGTTCCCG	120
Db		61	ACCCCTGCCTGCCGCAACCCCGGGCAGCCCGCGCGCGCCCGCCCGCGCAGCAGTTCCCG	120
Qy		121	CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG	180
Db		121	CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG	180
Qy		181	GTCACCAGCCAGGTCTTGCGGCTGGGCATCAACGGCAAAGTTTTGCAGATCTTCAACAAG	240
Db		181	GTCACCAGCCAGGTCTTGCGGCTGGGCATCAACGGCAAAGTTTTGCAGATCTTCAACAAG	240
Qy		241	AGGACCCAGGAGAAAATTGCGCCTCAAAATGCTTCAGGACTGCCCCAAGGCCCGCAGGGAG	300
Db		241	AGGACCCAGGAGAAAATTGCGCCTCAAAATGCTTCAGGACTGCCCCAAGGCCCGCAGGGAG	300
Qy		301	GTGGAGCTGCACTGGCGGGCCTCCAGTGCCCGCACATCGTACGGATCGTGGATGTGTAC	360
Db		301	GTGGAGCTGCACTGGCGGGCCTCCAGTGCCCGCACATCGTACGGATCGTGGATGTGTAC	360
Qy		361	GAGAAATCTGTACGCAGGGAGGAAGTGCTGTGATTGTTCATGGAATGTTTGGACGTGGA	420
Db		361	GAGAAATCTGTACGCAGGGAGGAAGTGCTGTGATTGTTCATGGAATGTTTGGACGTGGA	420
Qy		421	GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTACAGAAAGAGAAGCATCC	480
Db		421	GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTACAGAAAGAGAAGCATCC	480

RESULT 8
ADS84138
ID ADS84138 standard; cDNA; 1336 BP.
XX
XX AC ADS84138;
XX
DT 11-AUG-2005 (first entry)
XX
DE Human lymph node cDNA #1397.
XX
KW ss; gene; human; immunological response; blood cell; cancer;
KW immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;
KW bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
KW osteoporosis; pancreatitis; infection; arthritis; lymph node.
XX
OS Homo sapiens.
XX
PN US2004077003-A1.
XX
PD 22-APR-2004.
XX
PF 14-AUG-2003; 2003US-00641643.
XX

Qy	481	GAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTTGCCCAT	540
Db	481		
Qy	541	CGGGATGCAAGCCCTGAGAACTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA	600
Db	541	CGGGATGTCAGCCCTGAGAACTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA	600
Qy	601	CTCACTGACTTTGGCTTTGCCAAGGAAACCAACGACCCACAACTCTTTGACCACTCCTTGT	660
Db	601	CTCACTGACTTTGGCTTTGCCAAGGAAACCAACGACCCACAACTCTTTGACCACTCCTTGT	660
Qy	661	TATACACCGTACTATGTGGCTCCAGAAAGTCTGGGTCCAGAGAAGTATGACAAGTCTCTGT	720
Db	661	TATACACCGTACTATGTGGCTCCAGAAAGTCTGGGTCCAGAGAAGTATGACAAGTCTCTGT	720
Qy	721	GACATGTGGTCCCTGGGTGTCAATCATGTACATCTCTGTGTGTGGGTATCCCCCTTCTAC	780
Db	721	GACATGTGGTCCCTGGGTGTCAATCATGTACATCTCTGTGTGTGGGTATCCCCCTTCTAC	780
Qy	781	TCCAAACCAACCGGCCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAAATGGGCCAGTAT	840
Db	781	TCCAAACCAACCGGCCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAAATGGGCCAGTAT	840
Qy	841	GAATTTCCCAACCCAGAAATGGTTCAGAAATGATCAGAGGAAGTGAAGATGCTCATTCGGAAT	900
Db	841	GAATTTCCCAACCCAGAAATGGTTCAGAAATGATCAGAGGAAGTGAAGATGCTCATTCGGAAT	900
Qy	901	CTGCTGAAAAACAGAGCCCCACCCAGAGAATGACCATCACCGAGTTTATGAACACCCCTTGG	960
Db	901	CTGCTGAAAAACAGAGCCCCACCCAGAGAATGACCATCACCGAGTTTATGAACACCCCTTGG	960
Qy	961	ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCAAGCCGGTCTGTGAAGGAG	1020
Db	961	ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCAAGCCGGTCTGTGAAGGAG	1020
Qy	1021	GACAAGGACGGTGGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTTGGCCACAATGCGC	1080
Db	1021	GACAAGGACGGTGGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTTGGCCACAATGCGC	1080
Qy	1081	GTTGACTACGAGCAGATCAAGATATAAAGATTGAAGATGCATCCAAACCTCTGCTGCTG	1140
Db	1081	GTTGACTACGAGCAGATCAAGATATAAAGATTGAAGATGCATCCAAACCTCTGCTGCTG	1140
Qy	1141	AAGAGGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCACTGA	1191
Db	1141	AAGAGGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCACTGA	1191

ss; gene; human; immunological response; blood cell; cancer; immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis; bronchitis; ulcerative colitis; diabetes; multiple sclerosis; osteoporosis; pancreatitis; infection; arthritis; lymph node.

PR 09-FEB-1998; 98US-00023655.
XX (INCY-) INCYTE CORP.
PA Cocks BG, Stuart SG, Seilhamer JJ;
XX WPI; 2004-387937/36.
DR
XX
XX New compositions having a number of first, second and third
PT polynucleotide probes, useful in research and diagnostic applications in
PT cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
PT infections.
XX
PS Claim 15; SEQ ID NO 1397; 16pp; English.
XX
CC The invention relates to polynucleotides which are used as probes to
CC detect genes differentially expressed in an immunological response,
CC abundantly expressed in an immunological response and/or coding for a
CC polypeptide known to regulate blood cell biology. The polynucleotides are
CC useful in research and diagnostic applications particularly in cancer and
CC immunopathological conditions, such as AIDS, allergies, anaemia, asthma,
CC atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
CC sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
CC present sequence represents a human lymph node cDNA used to detect blood
CC cell and immunological response gene expression. Note: The present
CC sequence does not appear in the printed specification but was obtained in
CC electronic format from the USPTO web site
CC (seqdata.uspto.gov/sequence.html?DocID=20040077003).
XX
SQ Sequence 1336 BP; 338 A; 406 C; 340 G; 252 T; 0 U; 0 Other;
Query Match 99.2%; Score 1181.4; DB 13; Length 1336;
Best Local Similarity 99.5%; Pred. No. 2.7e-258;
Matches 1185; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCCCGCCCGCGCGCAGCCCCC 60
Db 1 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCCCGCCCGCGCGCAGCCCCC 60
QY 61 ACCCCTGCCCTGCCGACCCCCCGCGGCGAGCGCGCGCGCCCCCGCAGATTCCCG 120
Db 61 ACCCCTGCCCTGCCGACCCCCCGCGGCGAGCGCGCGCGCCCCCGCAGATTCCCG 120
QY 121 CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGACTACAAG 180
Db 121 CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGACTACAAG 180
QY 181 GTCACAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTTTGCAGATCTTCAACAAG 240
Db 181 GTCACAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTTTGCAGATCTTCAACAAG 240
QY 241 AGGACCCAGAGAAATTCCGCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 300
Db 241 AGGACCCAGAGAAATTCCGCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 300
QY 301 GTGGAGCTGCAGTGGCGGCTCCAGTGCGCGCACATCGTACGGATCGTGGATGTGTAC 360
Db 301 GTGGAGCTGCAGTGGCGGCTCCAGTGCGCGCACATCGTACGGATCGTGGATGTGTAC 360
QY 361 GAGAATCTGTACCGCAGGAGGAAGTGCCTGCTGATTGTCTATGGAATGTTTGGACGGTGA 420
Db 361 GAGAATCTGTACCGCAGGAGGAAGTGCCTGCTGATTGTCTATGGAATGTTTGGACGGTGA 420
QY 421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCAGAAAGAGAGCATCC 480
Db 421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCAGAAAGAGAGCATCC 480
QY 481 GAAATCATGAGAGCATCGGTAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 540
Db 481 GAAATCATGAGAGCATCGGTAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 540
QY 541 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 600
Db 541 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 600

Db 541 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 600
QY 601 CTCACTGACTTTGGCTTTGCCAAGGAAACACACAGCCACCAACTCTTTTGACCACCTCCTTGT 660
Db 601 CTCACTGACTTTGGCTTTGCCAAGGAAACACACAGCCACCAACTCTTTTGACCACCTCCTTGT 660
QY 661 TATACACCGTACTATGTGGTCCAGAAAGTGGTCCAGAGAAAGTATGACAAAGTCTCTGT 720
Db 661 TATACACCGTACTATGTGGTCCAGAAAGTGGTCCAGAGAAAGTATGACAAAGTCTCTGT 720
QY 721 GACATGTGGTCCCTGGGTGTCTCATGTATCATCTGCTGTGTGGGTATCCCCCTTCTAC 780
Db 721 GACATGTGGTCCCTGGGTGTCTCATGTATCATCTGCTGTGTGGGTATCCCCCTTCTAC 780
QY 781 TCCAACCCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
Db 781 TCCAACCCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
QY 841 GAATTTCCCAACCCAGAAATGGTCAAGAGTATCAGAGGAAGTGAAGTCTCATTCGGAAT 900
Db 841 GAATTTCCCAACCCAGAAATGGTCAAGAGTATCAGAGGAAGTGAAGTCTCATTCGGAAT 900
QY 901 CTGCTGAAAACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 960
Db 901 CTGCTGAAAACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 960
QY 961 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCCAGCCGGTCTCTGAAGGAG 1020
Db 961 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCCAGCCGGTCTCTGAAGGAG 1020
QY 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAGTGCCTTGGCCACAATCGC 1080
Db 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAGTGCCTTGGCCACAATCGC 1080
QY 1081 GTTGACTACGAGCAGATCAAGATAAAGATTGAAGATGATCAACACCTCTGTGCTGTG 1140
Db 1081 GTTGACTACGAGCAGATCAAGATAAAGATTGAAGATGATCAACACCTCTGTGCTGTG 1140
QY 1141 AAGAGCGGGAAGAAAGCTCGGGCCTGGAGGCTCGGGCTCTGGCCCACTGA 1191
Db 1141 AAGAGCGGGAAGAAAGCTCGGGCCTGGAGGCTCGGGCTCTGGCCCACTGA 1191
RESULT 9
AAF15803
ID AAF15803 standard; cDNA; 2802 BP.
XX
AC AAF15803;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:238.
XX
KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease; ss.
XX
OS Homo sapiens.
XX
PN WO200055174-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005988.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 1; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp polynucleotide of
CC the invention. Note: The sequence data for this patent is not represented
CC in the printed specification, but was obtained in electronic format
CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 2592 BP; 549 A; 763 C; 785 G; 495 T; 0 U; 0 Other;

Query Match 88.2%; Score 1050.4; DB 13; Length 2592;
Best Local Similarity 99.0%; Pred. No. 1.8e-228;
Matches 1057; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCCCGCGCCCGCGCAGCCCCC 60
DB 300 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCCCGCGCCCGCGCAGCCCCC 359

QY 61 ACCCCTGCCCTGCCGACCCCCCGCGCGAGCCGCGCGCCCGCGCAGGTTCCCG 120
DB 360 ACCCCTGCCCTGCCGACCCCCCGCGCGAGCCGCGCGCCCGCGCAGGTTCCCG 419

QY 121 CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 180
DB 420 CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 479

QY 181 GTCACCAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTTTGCAGATCTTCAACAAG 240
DB 480 GTCACCAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTTTGCAGATCTTCAACAAG 539

QY 241 AGGACCCAGGAGAAATTCCCTCAAATGTTTCAGGACTGCCCCAGAGCCCGCAGGGAG 300
DB 540 AGGACCCAGGAGAAATTCCCTCAAATGTTTCAGGACTGCCCCAGAGCCCGCAGGGAG 599

QY 301 GTGGAGCTGCACTGGCGGGCCTCCAGTGCOCGCACATCGTACGGATCGTGGATGTGTAC 360
DB 600 GTGGAGCTGCACTGGCGGGCCTCCAGTGCOCGCACATCGTACGGATCGTGGATGTGTAC 659

QY 361 GAGAATCTGTACGCAGGGAGGAAGTCCCTGCTGATTGTATGGAATGTTGGACGGTGA 420
DB 660 GAGAATCTGTACGCAGGGAGGAAGTCCCTGCTGATTGTATGGAATGTTGGACGGTGA 719

QY 421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGAGCATCC 480
DB 720 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGAGCATCC 779

QY 481 GAAATCATGAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 540
DB 780 GAAATCATGAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 839

QY 541 CGGGATGTCAAGCCTGAGAATCTCTTATACCTCAAAGGCCCAACGCCCATCTCTGAAA 600
DB 840 CGGGATGTCAAGCCTGAGAATCTCTTATACCTCAAAGGCCCAACGCCCATCTCTGAAA 899

QY 601 CTCACGTACTTTGGCTTTGCCAAGGAACACCAGCCACAACTCTTTGACCACTCCTTGT 660

DB 900 CTCACGTACTTTGGCTTTGCCAAGGAAACACCAGCCACAACCTCTTTGACCACTCCTTGT 959
QY 661 TATACACCGTACTATGTGGTCCAGAAAGTCTGGGTCCAGAGAAAGTATGACAAAGTCTCTGT 720
DB 960 TATACACCGTACTATGTGGTCCAGAAAGTCTGGGTCCAGAGAAAGTATGACAAAGTCTCTGT 1019
QY 721 GACATGTGGTCCCTGGGTGTTCATCATGTACATCTCTGTGTGGGTATCCCCCTTCTAC 780
DB 1020 GACATGTGGTCCCTGGGTGTTCATCATGTACATCTCTGTGTGGGTATCCCCCTTCTAC 1079
QY 781 TCCAACCAACGGCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
DB 1080 TCCAACCAACGGCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1139
QY 841 GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGTGCATTCGGAAT 900
DB 1140 GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGTGCATTCGGAAT 1199
QY 901 CTGCTGAAAACAGAGCCACCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 960
DB 1200 CTGCTGAAAACAGAGCCACCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 1259
QY 961 ATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCAGCCGGTCTCTGAAGGAG 1020
DB 1260 ATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCAGCCGGTCTCTGAAGGAG 1319
QY 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTG 1068
DB 1320 GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGTACCGGGCACTGG 1367

RESULT 11
ADV43402
ID ADV43402 standard; cDNA; 1113 BP.
XX
AC ADV43402;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1030.
XX
KW microarray; psychoneuroendocrinimmune; chronic fatigue;
KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO2004108899-A2.
XX
PD 16-DEC-2004.
XX
PF 04-JUN-2004; 2004WO-US017686.
XX
PR 04-JUN-2003; 2003US-0475915P.
XX
(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Nicholson A, Vernon SD;
XX
DR WPI; 2005-031682/03.
XX
PT New microarray comprising probes for genes involved in
PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
XX
PS Claim 1; SEQ ID NO 1030; 254pp; English.
XX
CC The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI
CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC cancer and infection. The present sequence represents a

CC	psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC	specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC	SEQ ID NO 1829 are provided.
XX	
SQ	Sequence 1113 BP; 276 A; 343 C; 286 G; 208 T; 0 U; 0 Other;
	Query Match 88.0%; Score 1048.4; DB 14; Length 1113;
	Best Local Similarity 99.9%; Pred. No. 4.1e-228;
	Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 TCCCAGGCGCAGAGCCCGCGGTGCCGTTCCCGCCCGCCCGCCCGCGCGCCCGCC 60
Db	13 TCCCAGGCGCAGAGCCCGCGGTGCCGTTCCCGCCCGCCCGCCCGCGCGCCCGCC 72
QY	61 ACCCCTGCCCTGCCGACCCCGCGCGCAGCCCGCGCGCCCGCGCGCAGTTCCCG 120
Db	73 ACCCCTGCCCTGCCGACCCCGCGCGCAGCCCGCGCGCCCGCGCGCAGTTCCCG 132
QY	121 CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 180
Db	133 CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 192
QY	181 GTCACCAAGCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTTGCAGATCTTCAACAAG 240
Db	193 GTCACCAAGCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTTGCAGATCTTCAACAAG 252
QY	241 AGGACCCAGGAGAAATTGCCCCCTCAAAATGTTTCAGGACTGCCCCAGGCCCGCAGGGAG 300
Db	253 AGGACCCAGGAGAAATTGCCCCCTCAAAATGTTTCAGGACTGCCCCAGGCCCGCAGGGAG 312
QY	301 GTGGAGCTGCACTGGCGGGCCTCCAGTGCCCGCACATCGTACGGATCGTGGATGTGTAC 360
Db	313 GTGGAGCTGCACTGGCGGGCCTCCAGTGCCCGCACATCGTACGGATCGTGGATGTGTAC 372
QY	361 GAGAACTCTGTACGAGGAGGAAGTGCCCTGTGATTGTTCATGGAATGTTGGACGGTGA 420
Db	373 GAGAACTCTGTACGAGGAGGAAGTGCCCTGTGATTGTTCATGGAATGTTGGACGGTGA 432
QY	421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAAGGCATTTCACAGAAAGAGAGCATCC 480
Db	433 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAAGGCATTTCACAGAAAGAGAGCATCC 492
QY	481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCTCAATCAACATTGCCCAT 540
Db	493 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCTCAATCAACATTGCCCAT 552
QY	541 CGGGATGTCAAGCCTGAGAAATCTCTTATACACTCCAAAAGGCCCAAAGCCCATCTTGA 600
Db	553 CGGGATGTCAAGCCTGAGAAATCTCTTATACACTCCAAAAGGCCCAAAGCCCATCTTGA 612
QY	601 CTCACGTACTTTGGCTTTGCCAAGGAACCAACGAGCCACAACTCTTTGACCACTCCTTGT 660
Db	613 CTCACGTACTTTGGCTTTGCCAAGGAACCAACGAGCCACAACTCTTTGACCACTCCTTGT 672
QY	661 TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCAGAGAAGTATGACAAAGTCCTGT 720
Db	673 TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCAGAGAAGTATGACAAAGTCCTGT 732
QY	721 GACATGTGGTCCCTGGGTGTCATCATGTACATCCTGCTGTGTGGGTATCCCCCCTTCTAC 780
Db	733 GACATGTGGTCCCTGGGTGTCATCATGTACATCCTGCTGTGTGGGTATCCCCCCTTCTAC 792
QY	781 TCCAAACCAACCGGCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
Db	793 TCCAAACCAACCGGCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 852
QY	841 GAATTTCCCAACCCAGAAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
Db	853 GAATTTCCCAACCCAGAAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 912
QY	901 CTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGG 960
Db	913 CTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGG 972

QY	961 ATCATGCAATCAACAAAGTCCCTCAAAACCCCACTGCACACGAGCCGGTCTCTGAAGGAG 1020
Db	973 ATCATGCAATCAACAAAGTCCCTCAAAACCCCACTGCACACGAGCCGGTCTCTGAAGGAG 1032
QY	1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAG 1050
Db	1033 GACAAGGAGCGGTGGGAGGATGTCAAGGGG 1062
	RESULT 12
ADP87584	
ID	ADP87584 standard; DNA; 1128 BP.
XX	
AC	ADP87584;
XX	
DT	23-SEP-2004 (first entry)
XX	
DE	Human NOVX polypeptide encoding DNA, NOV3d.
XX	
KW	anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;
KW	insulin resistance; hybridization probe; chromosome mapping;
KW	tissue typing; preventive medicine; pharmacogenomics; NOVX; human; gene;
XX	ds.
OS	Homo sapiens.
XX	
PN	WO2004056961-A2.
XX	
PD	08-JUL-2004.
XX	
PF	27-OCT-2003; 2003WO-US034114.
XX	
PR	25-OCT-2002; 2002US-0421239P.
PR	28-OCT-2002; 2002US-0421700P.
PR	31-OCT-2002; 2002US-0422776P.
PR	13-NOV-2002; 2002US-0426197P.
PR	20-DEC-2002; 2002US-0435498P.
PR	20-DEC-2002; 2002US-0435510P.
PR	20-DEC-2002; 2002US-0435568P.
PR	21-MAR-2003; 2003US-0456812P.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;
XX	
DR	WPI; 2004-500293/47.
DR	P-PSDB; ADP87585.
XX	
PT	New NOVX nucleic acid molecules and polypeptides useful for preventing or
PT	treating NOVX-associated disorders, e.g. diabetes, insulin resistance or
PT	obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX	
PS	Claim 1; SEQ ID NO 39; 570pp; English.
XX	
CC	The invention relates to a novel isolated nucleic acid molecule
CC	comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base
CC	pairs) fully defined in the specification; or encodes any of the amino
CC	acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the
CC	specification. The invention further comprises: an isolated polypeptide
CC	comprising any of the amino acid sequences cited above; a method for
CC	identifying compounds that modulate target polypeptide activity; an
CC	antibody that immunospecifically binds to the target polypeptide, where
CC	the target polypeptide comprises any of the above-mentioned amino acid
CC	sequences, an amino acid sequence that is at least 95% identical to the
CC	above amino acid sequences, an amino acid sequence of at least one domain
CC	of the above-mentioned amino acid sequences, or an amino acid sequence
CC	that is at least 95% identical to the domain of the above amino acid
CC	sequences; a method for identifying a potential therapeutic agent for use
CC	in treatment of a pathology, where the pathology is related to aberrant
CC	expression or aberrant physiological interactions of a target polypeptide
CC	; and a method of screening for a modulator of activity of or of latency
CC	or predisposition to a pathology associated with a target polypeptide.

CC The modulating compounds have anorectic and antidiabetic activities. The
CC nucleic acid sequences of the invention may be used in gene therapy to
CC treat disorders. The proteins of the invention may be used in creating a
CC vaccine. The composition and methods are useful for identifying compounds
CC that modulate protein activity or for diagnosing, preventing or treating
CC diverse pathological conditions, such as obesity, diabetes or insulin
CC resistance. The nucleic acids are also used as hybridization probes, in
CC chromosome mapping, tissue typing, preventive medicine, and
CC pharmacogenomics. This polynucleotide sequence represents the DNA
CC encoding a NOVX polypeptide of the invention.
XX
SQ

Sequence 1128 BP; 278 A; 349 C; 290 G; 211 T; 0 U; 0 Other;
Query Match 88.0%; Score 1048.4; DB 12; Length 1128;
Best Local Similarity 99.9%; Pred. No. 4.1e-228;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCAGGGCCAGAGCCCGCGGTTCGCGTTCGCGCCCGCGCCCGCGCGCAGCCCCC 60
Db |||||
28 TCCAGGGCCAGAGCCCGCGGTTCGCGTTCGCGCCCGCGCCCGCGCGCAGCCCCC 87
QY 61 ACCCCTGCCCTGCCGACCCCCCGCGCGAGCGCGCGCGCCCGCGCAGGATTCCCG 120
Db |||||
88 ACCCCTGCCCTGCCGACCCCCCGCGCGAGCGCGCGCGCCCGCGCAGGATTCCCG 147
QY 121 CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 180
Db |||||
148 CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 207
QY 181 GTCACCAAGCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTGGAGATCTTCAACAAG 240
Db |||||
208 GTCACCAAGCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTGGAGATCTTCAACAAG 267
QY 241 AGGACCCAGGAGAAATTGCCCCCTCAAAATGTTTCCAGGACTGCCCCAGGCCCGCAGGGAG 300
Db |||||
268 AGGACCCAGGAGAAATTGCCCCCTCAAAATGTTTCCAGGACTGCCCCAGGCCCGCAGGGAG 327
QY 301 GTGGAGTGCATGGCGGGCCTCCAGTGC CGCGCACATCGTACGGATCGTGGATGTGTAC 360
Db |||||
328 GTGGAGTGCATGGCGGGCCTCCAGTGC CGCGCACATCGTACGGATCGTGGATGTGTAC 387
QY 361 GAGAATCTGTACGAGGGAGGAAGTGCCTGCTGATTGTCTATGGAATGTTGGACGGTGA 420
Db |||||
388 GAGAATCTGTACGAGGGAGGAAGTGCCTGCTGATTGTCTATGGAATGTTGGACGGTGA 447
QY 421 GAACTCTTTAGCCGAATCCAGGATCGAGGACACAGGCATTCACAGAAAGAGAGCATCC 480
Db |||||
448 GAACTCTTTAGCCGAATCCAGGATCGAGGACACAGGCATTCACAGAAAGAGAGCATCC 507
QY 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGATTCATCAATCAACATTGCCCAT 540
Db |||||
508 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGATTCATCAATCAACATTGCCCAT 567
QY 541 CGGGATGTCAAGCCTGAGAAATCTTTATACACCTCCAAAAGGCCAACGCCATCCTGAAA 600
Db |||||
568 CGGGATGTCAAGCCTGAGAAATCTTTATACACCTCCAAAAGGCCAACGCCATCCTGAAA 627
QY 601 CTCACGTGACTTTGGCTTTGCCAAGGAAACACAGCCACAACCTTTTGACCACTCCTTGT 660
Db |||||
628 CTCACGTGACTTTGGCTTTGCCAAGGAAACACAGCCACAACCTTTTGACCACTCCTTGT 687
QY 661 TATACACCGTACTATGTGGCTCCAGAGTGTGGTCCAGAGAGTATGACAAGTCTCTGT 720
Db |||||
688 TATACACCGTACTATGTGGCTCCAGAGTGTGGTCCAGAGAGTATGACAAGTCTCTGT 747
QY 721 GACATGTGTGCTGGGTGTATCATGTATCATCTCTGTGTGGGTATCCCCCCTTCTAC 780
Db |||||
748 GACATGTGTGCTGGGTGTATCATGTATCATCTCTGTGTGGGTATCCCCCCTTCTAC 807
QY 781 TCCAACCAAGCGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
Db |||||
808 TCCAACCAAGCGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 867

QY 841 GAATTTCCCAACCCAGAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
Db |||||
868 GAATTTCCCAACCCAGAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 927
QY 901 CTGCTGAAAACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGG 960
Db |||||
928 CTGCTGAAAACAGAGCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGG 987
QY 961 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCAAGGTCCTGAAGGAG 1020
Db |||||
988 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCAAGGTCCTGAAGGAG 1047
QY 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAG 1050
Db |||||
1048 GACAAGGAGCGGTGGGAGGATGTCAAGGGG 1077

RESULT 13
ABL67227
ID ABL67227 standard; DNA; 2258 BP.

XX ABL67227;
XX
DT 15-MAY-2002 (first entry)
XX

Thyroid cancer related gene sequence SEQ ID NO:5564.

Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
gene; ds.

OS Homo sapiens.

PN WO200194629-A2.

XX
PD 13-DEC-2001.

XX
PF 30-MAY-2001; 2001WO-US010838.

XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.

PI Au-Young J, Seilhamer JJ;
XX WPI; 2003-352189/33.
DR Combination of polynucleotide probes, useful as array elements in a
XX microarray for monitoring the expression of a number of target
PT polynucleotides.
PT Claim 1; SEQ ID NO 1415; 65pp; English.
XX
PS
XX The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC segdata.uspto.gov/sequence.html?DocID=06500938B1
XX
SQ Sequence 2258 BP; 496 A; 711 C; 618 G; 433 T; 0 U; 0 Other;

Query Match 88.0%; Score 1048.4; DB 10; Length 2258;
Best Local Similarity 99.9%; Pred. No. 5e-228;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCCCGCCCGCCGCGCAGCCCCC 60
DB 391 TCCAGGGCCAGAGCCCGCGGTGCCGTTCCCGCCCCCGCCCGCCGCGCAGCCCCC 450
QY 61 ACCCTGCCCTGCCGACCCCCCGCGCAGCCCGCGCCCGCCCCCGCAGCAGTTCCCG 120
DB 451 ACCCTGCCCTGCCGACCCCCCGCGCAGCCCGCGCCCGCCCCCGCAGCAGTTCCCG 510
QY 121 CAGTTCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 180
DB 511 CAGTTCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 570
QY 181 GTCACCAAGCCAGGTCTCTGGGCTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG 240
DB 571 GTCACCAAGCCAGGTCTCTGGGCTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG 630
QY 241 AGGACCCAGGAGAAATTGCCCCCTCAAAATGCTTCAGGACTGCCCCCAAGSCCCGCGAGGAG 300
DB 631 AGGACCCAGGAGAAATTGCCCCCTCAAAATGCTTCAGGACTGCCCCCAAGSCCCGCGAGGAG 690
QY 301 GTGGAGCTGCACCTGGCGGGCCCTCCCAGTGGCCGCACATCGTACGGATCGTGGATGTGTAC 360
DB 691 GTGGAGCTGCACCTGGCGGGCCCTCCCAGTGGCCGCACATCGTACGGATCGTGGATGTGTAC 750
QY 361 GAGAAATCTGTACGAGGGAGGAAGTGCCCTGCTGATTTGTATGGAATGTTGGACGGTGA 420
DB 751 GAGAAATCTGTACGAGGGAGGAAGTGCCCTGCTGATTTGTATGGAATGTTGGACGGTGA 810
QY 421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTCACAGAAGAGAGCATCC 480
DB 811 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTCACAGAAGAGAGCATCC 870
QY 481 GAAATCATGAAGAGCATCGGTGAGGCCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 540
XX

DB 871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT 930
QY 541 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 600
DB 931 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 990
QY 601 CTCACCTGACTTTGGCTTTGCCAAGGAAACACACAGCCACAACCTCTTTGACCACCTCCTTGT 660
DB 991 CTCACCTGACTTTGGCTTTGCCAAGGAAACACACAGCCACAACCTCTTTGACCACCTCCTTGT 1050
QY 661 TATACACCGTACTATGTGGCTCCAGAAAGTCTCTGGGTCCAGAGAAAGTATGACAAAGTCTGT 720
DB 1051 TATACACCGTACTATGTGGCTCCAGAAAGTCTCTGGGTCCAGAGAAAGTATGACAAAGTCTGT 1110
QY 721 GACATGTGTCCTGGGTGTCATCATGTATCATCTCTGCTGTGGGTATCCCCCCTTCTAC 780
DB 1111 GACATGTGTCCTGGGTGTCATCATGTATCATCTCTGCTGTGGGTATCCCCCCTTCTAC 1170
QY 781 TCCAACCAACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
DB 1171 TCCAACCAACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
QY 841 GAATTTCCCAACCCAGAAATGGTCAGAACTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
DB 1231 GAATTTCCCAACCCAGAAATGGTCAGAACTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
QY 901 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGG 960
DB 1291 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCCCTTGG 1350
QY 961 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCCAGCCGGTCTCTGAAGGAG 1020
DB 1351 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCCAGCCGGTCTCTGAAGGAG 1410
QY 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAG 1050
DB 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGG 1440

RESULT 15
ADI56613
ID ADI56613 standard; DNA; 2258 BP.
XX
AC ADI56613;
XX
DT 22-APR-2004 (first entry)
XX
DE Human polynucleotide probe #1415.
XX
KW Human; probe; ss; receptor-like polypeptide; transducing polypeptide;
KW effector-like polypeptide; cancer; immunopathology; neuropathology;
KW drug development; toxicology; carcinogenicity;
KW signalling pathway polypeptide; adrenal gland; bladder; bone;
KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;
KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.
XX
OS Homo sapiens.
XX
PN US2004010136-A1.
XX
PD 15-JAN-2004.
XX
PF 26-NOV-2002; 2002US-00305720.
XX
PR 30-JAN-1998; 98US-00016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Au-Young J, Seilhamer JJ;
XX WPI; 2004-090520/09.
XX

PT New composition comprising polynucleotide probes, useful as array
PT elements in a microarray for monitoring the expression of target
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
PT fragments.
XX
PS Claim 6; SEQ ID NO 1415; 73pp; English.
XX
XX
CC The invention relates to a composition of polynucleotide probes
CC comprising first polynucleotide probes comprising at least a portion of a
CC gene encoding a receptor-like polypeptide, second polynucleotide probes
CC comprising at least a portion of a gene encoding a transducing
CC polypeptide and third polynucleotide probes comprising at least a portion
CC of a gene encoding an effector-like polypeptide. The probes of the
CC composition are useful as array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray is useful in the
CC diagnosis and treatment of cancer, an immunopathology or a
CC neuropathology. It can also be used for drug discovery and development,
CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.
CC Microarrays can also be used for monitoring the progression of diseases
CC that may be associated with the altered expression of signalling pathway
CC polypeptides. The composition can also be used to purify a subpopulation
CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of
CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
CC epilepsy, Alzheimer's disease or depression. This sequence represents a
CC human polynucleotide probe of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX

SQ Sequence 2258 BP; 496 A; 711 C; 618 G; 433 T; 0 U; 0 Other;

Query Match 88.0%; Score 1048.4; DB 12; Length 2258;

Best Local Similarity 99.9%; Pred. No. 5e-228;

Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	TCCCAGGGCCAGACCCCGCGGTGCGTTCCTCCCGCCCCGGCCCCCGCGCAGCCCCC	60
Db	391		
		TCCCAGGGCCAGACCCCGCGGTGCGTTCCTCCCGCCCCGGCCCCCGCGCAGCCCCC	450
Qy	61	ACCCCTGCCCTGCCGACCCCCCGGGCGCAGCCGCGCGCGCCCCCGCAGCAGTTCCCG	120
Db	451		
		ACCCCTGCCCTGCCGACCCCCCGGGCGCAGCCGCGCGCGCCCCCGCAGCAGTTCCCG	510
Qy	121	CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG	180
Db	511		
		CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG	570
Qy	181	GTCAACAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG	240
Db	571		
		GTCAACAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG	630
Qy	241	AGGACCCAGGAGAAATTGCGCCCTCAAAATGCTCAGGACTGCCCCCAAGSCCGCAGGGAG	300
Db	631		
		AGGACCCAGGAGAAATTGCGCCCTCAAAATGCTCAGGACTGCCCCCAAGSCCGCAGGGAG	690
Qy	301	GTGGAGCTGCACCTGSCGGGCCTCCCAGTGCCTCCGACATCGTACGGATCGTGGATGTGTAC	360
Db	691		
		GTGGAGCTGCACCTGSCGGGCCTCCCAGTGCCTCCGACATCGTACGGATCGTGGATGTGTAC	750
Qy	361	GAGAAATCTGTACGCAGGAGGAAGTGCCTGTGATTTGTCATGGAATGTTGGACGGTGGG	420
Db	751		
		GAGAAATCTGTACGCAGGAGGAAGTGCCTGTGATTTGTCATGGAATGTTGGACGGTGGG	810
Qy	421	GAACTCTTTAGCCGAATCCAGGATCGAGGAGACGAGGCATTCACAGAAAGAGCATCC	480
Db	811		
		GAACTCTTTAGCCGAATCCAGGATCGAGGAGACGAGGCATTCACAGAAAGAGCATCC	870
Qy	481	GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT	540
Db	871		
		GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT	930

Search completed: June 19, 2006, 16:04:09

Job time : 850 secs

Qy	541	CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA	600
Db	931		
		CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA	990
Qy	601	CTCACTGACTTTGGCTTTGCCAAGGAAAACCCAGCCCACTCTTTGACCACCTCCTTGT	660
Db	991		
		CTCACTGACTTTGGCTTTGCCAAGGAAAACCCAGCCCACTCTTTGACCACCTCCTTGT	1050
Qy	661	TATACACCGTACTATGTGGCTCCAGAAGTGTGGGTCCAGAGAAGTATGACAAAGTCTGT	720
Db	1051		
		TATACACCGTACTATGTGGCTCCAGAAGTGTGGGTCCAGAGAAGTATGACAAAGTCTGT	1110
Qy	721	GACATGTGGTCCCTGGGTGTATCATGTATCATCTCTGTGTGGGTATCCCCCTTCTAC	780
Db	1111		
		GACATGTGGTCCCTGGGTGTATCATGTATCATCTCTGTGTGGGTATCCCCCTTCTAC	1170
Qy	781	TCCAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT	840
Db	1171		
		TCCAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT	1230
Qy	841	GAATTTCCAAACCCAGAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT	900
Db	1231		
		GAATTTCCAAACCCAGAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT	1290
Qy	901	CTGCTGAAAACAGAGCCCAACCCAGAGAATGACCATCACCGAGTTTATGAACCCCTTGG	960
Db	1291		
		CTGCTGAAAACAGAGCCCAACCCAGAGAATGACCATCACCGAGTTTATGAACCCCTTGG	1350
Qy	961	ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACACCGCGGTCTCTGAAGGAG	1020
Db	1351		
		ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACACCGCGGTCTCTGAAGGAG	1410
Qy	1021	GACAAGGAGCGGTGGGAGGATGTCAAGGAG	1050
Db	1411		
		GACAAGGAGCGGTGGGAGGATGTCAAGGAG	1440

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OM nucleic - nucleic search, using sw model

Run on: June 19, 2006, 15:52:45 ; Search time 6434 Seconds
(without alignments)
10351.247 Million cell updates/sec

Title: US-10-469-221-1
Perfect score: 1191
Sequence: 1 tccaggccagagccgcc.....ctgcggctctggccactga 1191

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Length DB ID Description
1	928.4	78.0	2674 6 AK155171 Mus muscu
2	894.8	75.1	901 8 CR980921 CR980921
3	780	65.5	780 14 AY410229 AY410229
4	755.6	63.4	850 9 DN107605 DN107605
5	742.6	62.4	941 3 BQ884713 BQ884713
6	737.6	61.9	785 2 BG397545 BG397545
7	715	60.0	726 8 CN431763 CN431763
8	710	59.6	710 10 DR423458 DR423458
9	710	59.6	756 8 CV804995 CV804995
10	688	57.8	720 2 BG779875 BG779875
11	678	56.9	902 10 DV928789 DV928789
12	663.2	55.7	780 14 AY410231 AY410231
13	660.4	55.4	855 8 CO399284 CO399284
14	652.6	54.8	1048 2 BG106843 BG106843
15	652.2	54.8	776 3 BU609266 BU609266
16	649.8	54.6	842 5 CF617043 CF617043
17	646.4	54.3	654 8 CN431764 CN431764
18	644.6	54.1	803 5 CF725030 CF725030
19	641.6	53.9	651 4 CB043982 CB043982

20	641	53.8	858	8	CO394436	CO394436	AGENCOURT
21	637.6	53.5	945	2	BG421869	BG421869	602449607
22	636.6	53.5	825	7	BF309820	BF309820	601892475
23	635.4	53.4	751	4	CB169658	CB169658	RUC603000
24	634.4	53.3	846	2	BG480613	BG480613	602527051
25	624.8	52.5	827	9	DN284271	DN284271	1184539 M
26	620	52.1	778	8	CO246458	CO246458	AGENCOURT
27	615.4	51.7	909	7	BE876507	BE876507	601486252
28	613.4	51.5	696	1	AI478890	AI478890	tm25b05.x
29	611.2	51.3	752	8	CK974173	CK974173	4104800 B
30	604.6	50.8	728	5	CF725542	CF725542	UI-M-GZ0-
31	604.4	50.7	727	8	CV783919	CV783919	UI-M-HY0p
32	601.2	50.5	642	7	BE280175	BE280175	601158383
33	596.2	50.1	875	5	CF582482	CF582482	AGENCOURT
34	594.2	49.9	915	3	BQ964944	BQ964944	AGENCOURT
35	591.4	49.7	690	7	AW918725	AW918725	EST350029
36	590.8	49.6	675	3	BU671169	BU671169	NISC_lr05
37	585.6	49.2	729	9	DN933930	DN933930	AGENCOURT
38	585.2	49.1	739	2	BI077614	BI077614	602871715
39	583.6	49.0	690	10	DY113286	DY113286	000311BSP
40	582	48.9	663	10	DT824579	DT824579	LB00234.C
41	581.6	48.8	764	2	BI150810	BI150810	602914708
42	579.8	48.7	1182	9	DN666480	DN666480	CFW32-D05
43	576.6	48.4	789	9	DN872742	DN872742	nad22b02.
44	574.8	48.3	648	7	AW071750	AW071750	ws55b11.x
45	573.6	48.2	653	10	DT828222	DT828222	LB00256.C

ALIGNMENTS

RESULT 1

AK155171 2674 bp mRNA linear HTC 21-SEP-2005

LOCUS Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630205L24 product:MAP kinase-activated protein kinase 2, full insert sequence.

ACCESSION AK155171

VERSION AK155171.1 GI:74199084

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 10349636

REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 11042159

REFERENCE 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 11076861

REFERENCE 4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,

Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,C., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

11217851

5

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasaki,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Sempile,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

FANTOM Consortium

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420 (6915), 563-573 (2002)

12466851

6

Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C., Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R., Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R., Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E., Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L., Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M., Chiu,K.P., Choudhary,V., Christoffels,A., Clutterbuck,D.R., Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G., di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G., Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M., Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E., Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N., Hill,D., Huminecki,L., Iacono,M., Kawasaki,Y., Kelso,J., Ishikawa,T., Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelsø,J., Kitamura,H., Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K., Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J., Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L., Matsuda,H., Matsuzawa,S., Miki,H., Mignone,F., Miyake,S.,

Morris,K., Mottagui-Tabar,S., Mulder,N., Nakano,N., Nakauchi,H., Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O., Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G., Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z., Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A., Schneider,C., Schonbach,C., Sekiguchi,K., Sempile,C.A., Seno,S., Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D., Sinclair,B., Sperling,S., Stupka,E., Sugiyura,K., Sultana,R., Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S., Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R., Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A., Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T., Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A., Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M., Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M., Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M., Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M., Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K., Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.

FANTOM Consortium

The transcriptional landscape of the mammalian genome

Science 309 (5740), 1559-1563 (2005)

16141072

7

Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T., Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlestedt,C.

RIKEN Genome Exploration Research Group

Antisense transcription in the mammalian transcriptome

Science 309 (5740), 1564-1566 (2005)

16141073

8 (bases 1 to 2674)

Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,J., Kojima,M., Konno,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submission

Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/

URL:http://fantom.gsc.riken.jp/.

Location/Qualifiers

1. .2674

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286. .1446

CDS

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Qy	158	ACGCCATCATCGATGACTACAAGGTCAACGACGAGGTCCCTGGGGTGGGCTCAACGGCA	217		
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EST.				
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE				
AUTHORS				
Heil,O., Ebert,L., Hennig,S., Henze,S., Radelof,U., Schneider,D. and Korn,B.				
TITLE				
Human T-Lymphocytes library				
JOURNAL				
Unpublished (2005)				
COMMENT				
Contact: Inge Arlart				
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH				
Heubnerweg 6, D-14059 Berlin, Germany				
Email: www.rzpd.de				
RZPD; RZPDp9016G1344.				
RZPDLIB; (Human T-Lymphocytes) RZPD LIB No.9016				
http://www.rzpd.de/cgi-bin/products/set.cgi?libNo=9016 Contact: Inge Arlart				
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH				
Heubnerweg 6, D-14059 Berlin, Germany				
Tel: +49 30 32639 100				
Fax: +49 30 32639 111				
www.rzpd.de				
This clone is available from RZPD;				
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDp9016G1344				
contact RZPD (product- support@rzpd.de) for further information.				
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LOCUS
DEFINITION 1105067 MARC 4PIG Sus scrofa cDNA 5', mRNA linear EST 14-FEB-2005
ACCESSION DN107605
VERSION DN107605.1 GI:59782868
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SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
1 (bases 1 to 850)
Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
Nonneman,D.J., Wray,J.E. and Keele,J.W.
Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: HHY8003 row: B column: 15
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RESULT 5
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DEFINITION BQ884713 941 bp mRNA linear EST 16-AUG-2002
ACCESSION BQ884713
VERSION BQ884713.1 GI:22276731

KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 941)
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
Ph.D.
cDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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Db 481 GTAAGACAAGTCCTGTGACATGTGGTCCTTGGGTGTCATCATGTATATTTGCTGTGG 540
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QY 885 GATGCTCATTCGGAATCTGCTGAAAAACAGAGCCCCACCCAGAGAATGACCATCACCGAGTT 944
Db 661 GATGCTTATCCGGAATCTGCTAAAAAACAGAGCCCCACCCAGAGAATGACCATCACAGAATT 720
QY 945 TATGAACCAACCCCTTGGATCATGCAATCAACAAGGTCCCTCAAACCCCACTGCACACCAG 1004
Db 721 CATGAACCAACCCCTTGGATCATGCAATCTACGAAGTCCCTCAGACTCCACTGCACACCAG 780
QY 1005 CCGG-GTCCTGAAGGAGGACAAAGAGCGG-TGGGAGGATGTCAAGGA-GGAGATGACCAG 1061
Db 781 CCNGTGTCTTGAAGGAGGACAAAGAACCGGATGGGAGGATGTCAAGGAGGAGATGACCAG 840
QY 1062 TGCCTT-GGCCACAATCGCGTTGACTACGAGCAGATCAAGATAFAAAAAAGATTGAAGATG 1120
Db 841 TGCCCTTGGGCCACGATCGCTGTGACTATGAGCAGATCCAGATAAAGAAGATAGAAGACG 900
QY 1121 CATCCAACCCCTCTGCTGCTGAAGAGCGGGAAGAA 1154
Db 901 CATCCAACCCCTCTGCTTCTCAAGAGCGGGAAGAA 934
RESULT 6
BG397545
LOCUS BG397545 785 bp mRNA linear EST 12-MAR-2001
DEFINITION 602439376F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565442 5',
mRNA sequence.
ACCESSION BG397545
VERSION BG397545.1 GI:13290993
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 785)
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM1282 row: h column: 19
High quality sequence stop: 761.
FEATURES
source
1. .785
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4565442"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 61.9%; Score 737.6; DB 2; Length 785;
Best Local Similarity 98.3%; Pred. No. 9.6e-170;
Matches 767; Conservative 0; Mismatches 9; Indels 4; Gaps 2;
QY 272 TTCAGGACTGCCCAAGCCCGCAGGAGGTGGAGCTGCACTGGCGGCCTCCAGTGCC 331
Db 2 TTCAGGACTGCCCAAGCCCGCAGGAGGTGGAGCTGCACTGGCGGCCTCCAGTGCC 61
QY 332 CGCACATCGTACGGATCGTGGATGTGTACGAGAACTCTGTACGCAGGGAGGAAGTGCCTGC 391
Db 62 CGCACATCGTACGGATCGTGGATGTGTACGAGAACTCTGTACGCAGGGAGGAAGTGCCTGC 121
QY 392 TGATTGTCATGGAATGTTGGACGGTGGAGAACTCTTTAGCCGAATCCAGGATCGAGGAG 451
Db 122 TGATTGTCATGGAATGTTGGACGGTGGAGAACTCTTTAGCCGAATCCAGGATCGAGGAG 181
QY 452 ACCAGGCATTACAGAAAGAGAAGCATCCGAAATCATGAAGAGCATCGGTGAGGCCATCC 511
Db 182 ACCAGGCATTACAGAAAGAGAAGCATCCGAAATCATGAAGAGCATCGGTGAGGCCATCC 241
QY 512 AGTATCTGCATTCAATCAACATTTGCCCATCGGCATCGGAGTGTCAAGCCTGAGAACTCTTTATACA 571
Db 242 AGTATCTGCATTCAATCAACATTTGCCCATCGGCATCGGAGTGTCAAGCCTGAGAACTCTTTATACA 301
QY 572 CCTCCAAAAGGCCCAAGCCCATCTCTGAAACTCACTGACTTTGGCTTTGCCAAGGAAACCA 631
Db 302 CCTCCAAAAGGCCCAAGCCCATCTCTGAAACTCACTGACTTTGGCTTTGCCAAGGAAACCA 361
QY 632 CCAGCCACAACCTCTTGACCACTCCTTGTATACACCGTACTATGTGGTCCAGAAAGTGC 691
Db 362 CCAGCCACAACCTCTTGACCACTCCTTGTATACACCGTACTATGTGGTCCAGAAAGTGC 421
QY 692 TGGTCCAGAGAAAGTATGACAAAGTCTGTGACATGTGTCCTCGGTGTGTCATGATACA 751
Db 422 TGGTCCAGAGAAAGTATGACAAAGTCTGTGACATGTGTCCTCGGTGTGTCATGATACA 481
QY 752 TCCTGCTGTGGGTATCCCCCTTCTACTCCAAACAGGCGCTTGCCATCTCTCCGGGCA 811
Db 482 TCCTGCTGTGGGTATCCCCCTTCTACTCCAAACAGGCGCTTGCCATCTCTCCGGGCA 541
QY 812 TGAAGACTCGCATCCGAATGGCCAGTATGAATTTCCCAACCCAGAAATGCTCAGAAATAT 871
Db 542 TGAAGACTCGCATCCGAATGGCCAGTATGAATTTCCCAACCCAGAAATGCTCAGAAATAT 601
QY 872 CAGAGGAAGTGAAGATGCTCATTCGGAATCTGCTGAAACACAGAGCCCAACCCAGAGAATGA 931
Db 602 CAGAGGAAGTGAAGATGCTCATTCGGAATCTGCTGAAACACAGAGCCCAACCCAGAGAATGA 661
QY 932 CCATCACCGAGTTTATGAACCCACCTTGGATCATGCAATCAACAAAGGTCCCTCAAACCC 991
Db 662 CCATCACCGAGTTTATGAACCA - CCTTGGATCATGCAATCAACAAAGGTCCCTCAAACCC 720
QY 992 CACTGCACACACCGCGGTCTGAAGGAGGACAAGGAGCGGTGGGAGGATGTCAAGGAGG 1051
Db 721 AATGACA --- CCAGCGGGTCTCTGAAGGAGGACAAGGAGCGGTGGGAGGATGTCAAGGAGG 777

RESULT 7

CN431763
LOCUS CN431763 726 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000600180477 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN431763
VERSION CN431763.1 GI:47419357
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 726)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.

TITLE

Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation

JOURNAL
PUBMED
COMMENT

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R
Regenerative Medicine
Geron Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbrandenberger@geron.com

Insert Length: 726 Std Error: 0.00.

FEATURES
source

Location/Qualifiers
1..726
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7"
/clone_lib="GRN_PRENEU"
/note="Oligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic acid and mitogens."

ORIGIN

Query Match 60.0%; Score 715; DB 8; Length 726;
Best Local Similarity 99.3%; Pred. No. 3.3e-164;
Matches 718; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 294 CAGGGAGGTGGAGCTGCACCTGGCGGCTCCAGTCCCGCACATCGTACGGATCGTGGA 353
Db 4 CAGGGAGGTGGAGCTGCACCTGGCGGCTCCAGTCCCGCACATCGTACGGATCGTGGA 63
QY 354 TGTGTACGAGAACTCTGTACGCAGGAGGAAGTGCCTGCTGATGTCATGGAATGTTTGA 413
Db 64 TGTGTACGAGAACTCTGTACGCAGGAGGAAGTGCCTGCTGATGTCATGGAATGTTTGA 123
QY 414 CGGTGGAGAACTCTTTAGCCGAATCCAGGATCGAGGAGACCGAGCATTCACAGAAAGAGA 473
Db 124 CGGTGGAGAACTCTTTAGCCGAATGGGGGATCGAGGAGACCGAGCATTCACAGAAAGAGA 183
QY 474 AGCATCCGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAACAT 533
Db 184 AGCATCCGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAACAT 243
QY 534 TGCCCATCGGGATGTCAAGCCTGAGAATCTTTATACACCTCCAAAAGGCCCAACGCCAT 593
Db 244 TGCCCATCGGGATGTCAAGCCTGAGAATCTTTATACACCTCCAAAAGGCCCAACGCCAT 303
QY 594 CCTGAAACTCACTGACTTTGGCTTTGCCAAGGAAACCCAGCCACAACACTCTTTGACCCAC 653
Db 304 CCTGAAACTCACTGACTTTGGCTTTGCCAAGGAAACCCAGCCACAACACTCTTTGACCCAC 363
QY 654 TCCTTGTATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAAGTATGACAA 713
Db 364 TCCTTGTATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAAGTATGACAA 423
QY 714 GTCCTGTGACATGTGTCCTCGGTGTGTCATGATCATCTGCTGTGTGGGTATCCCCC 773
Db 424 GTCCTGTGACATGTGTCCTCGGTGTGTCATGATCATCTGCTGTGTGGGTATCCCCC 483
QY 774 CTTCTACTCCAAACACCGCCCTTGCCATCTCTCCGGGCGATGAAGACTCGCATCCGAATGGG 833
Db 484 CTTCTACTCCAAACACCGCCCTTGCCATCTCTCCGGGCGATGAAGACTCGCATCCGAATGGG 543

QY 834 CCAGTATGAATTTCCCAACCCAGAAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCAT 893
|||||
Db 544 CCAGTATGAATTTCCCAACCCAGAAATGGTCAGAAGTATCAGAGGAAGTGAAGATGCTCAT 603

QY 894 TCGGAATCTGCTGAAAAACAGAGCCCAACCCAGAGAATGACCATCACCGAGTTTATGAACCA 953
|||||
Db 604 TCGGAATCTGCTGAAAAACAGAGCCCAACCCAGAGAATGACCATCACCGAGTTTATGAACCA 663

QY 954 CCCTTGGATCATGCAATCAACAAAGGTCCTCAAAACCCCACTGCACACAGCCGGGTCTT 1013
|||||
Db 664 CCCTTGGATCATGCAATCAACAAAGGTCCTCAAAACCCCACTGCACACAGCCGGGTCTT 723

QY 1014 GAA 1016
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Db 724 GAA 726

RESULT 8
DR423458
LOCUS
DEFINITION nav26d01.y1 Human pterygium. Unnormalized (nav) Homo sapiens cDNA
clone nav26d01 5', mRNA sequence.

ACCESSION DR423458
VERSION DR423458.1 GI:68325474
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 710)
AUTHORS Wistow,G., Jaworski,C., Aryankalayil-John,M., Rowsey,J.J., Cox,C.,
Reid,T., Dushku,N. and Carper, D.
TITLE NEiBank analysis of Human pterygium
JOURNAL Unpublished (2005)
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 26 row: d column: 01
Seq primer: Universal M13 Reverse.

FEATURES
source
1..710
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="nav26d01"
/tissue_type="pterygium"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human pterygium. Unnormalized (nav)"
/note="Organ: Eye; Vector: pCMVSPORT6; RNA was extracted
from 9 pooled human pterygia. A directionally cloned cDNA
library in the pCMVSPORT6 vector (Invitrogen) was
constructed at Bioserve Biotechnology (Laurel MD)
essentially following the protocols of the SuperScript
Plasmid System, full details of which are contained in the
manufacturer's instruction manual
(http://www.lifetech.com/). First strand synthesis was
carried out using a Not I primer-adaptor
[5'-pGACTAGTTCTAGATCGGAGCGCGCCC(T)15-3']. cDNA was
cloned in Not I/Sal I sites. EST analysis was performed at
the NIH Intramural Sequencing Center (NISC). Analyzed data
available through http://neibank.nei.nih.gov."

ORIGIN

Query Match 59.6%; Score 710; DB 10; Length 710;
Best Local Similarity 100.0%; Pred. No. 5.5e-163;
Matches 710; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 GCCGCAGCCCCCCCCCTGCCCCGCGCACCCCCCGCGCGCAGCGCGCGCCCCC 107
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Db 1 GCCGCAGCCCCCCCCCTGCCCCGCGCACCCCCCGCGCGCAGCGCGCCCCC 60

QY 108 GCAGCAGTTCCCGCAGTTCCACGTCAAGTCCGGCTGCAGATCAAGAAGAACGCCATCAT 167
|||||
Db 61 GCAGCAGTTCCCGCAGTTCCACGTCAAGTCCGGCTGCAGATCAAGAAGAACGCCATCAT 120

QY 168 CGATGACTACAAGGTCAACGAGCCAGGTCTTGGGGCTGGGCATCAACGGCAAGTTTGTGA 227
|||||
Db 121 CGATGACTACAAGGTCAACGAGCCAGGTCTTGGGGCTGGGCATCAACGGCAAGTTTGTGA 180

QY 228 GATCTTCAACAAGAGGAGCCAGGAGAAAATTGCCCCCTCAAAAATGTTTCAGGACTGCCCCAA 287
|||||
Db 181 GATCTTCAACAAGAGGAGCCAGGAGAAAATTGCCCCCTCAAAAATGTTTCAGGACTGCCCCAA 240

QY 288 GGCCCGCAGGGAGGTGGAGCTGCACTGGCGGGCCCTCCAGTGCCTGCACATCGTACGGAT 347
|||||
Db 241 GGCCCGCAGGGAGGTGGAGCTGCACTGGCGGGCCCTCCAGTGCCTGCACATCGTACGGAT 300

QY 348 CGTGGATGTGTACGAGAATCTGTACGAGGGAGGAAGTGCCTGTGATTGTTCATGGAATG 407
|||||
Db 301 CGTGGATGTGTACGAGAATCTGTACGAGGGAGGAAGTGCCTGTGATTGTTCATGGAATG 360

QY 408 TTTGGACGGTGGAGAACTCTTTAGCCGAATCCAGGATCGAGGAGACCGAGCATTCACAGA 467
|||||
Db 361 TTTGGACGGTGGAGAACTCTTTAGCCGAATCCAGGATCGAGGAGACCGAGCATTCACAGA 420

QY 468 AAGAGAAGCATCCGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAAT 527
|||||
Db 421 AAGAGAAGCATCCGAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAAT 480

QY 528 CAACATTGCCCATCGGGATGTCAAGCTGAGAATCTCTTATACACCTCCAAAAGGCCCAA 587
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Db 481 CAACATTGCCCATCGGGATGTCAAGCTGAGAATCTCTTATACACCTCCAAAAGGCCCAA 540

QY 588 CGCCATCCTGAAACTCACTGACTTTGGCTTTGCCAAGGAAACCAACAGCCACAACTCTTT 647
|||||
Db 541 CGCCATCCTGAAACTCACTGACTTTGGCTTTGCCAAGGAAACCAACAGCCACAACTCTTT 600

QY 648 GACCACCTCTTGTATATACACCGTACTATGTGGTCCAGAAAGTGTGGTCCAGAGAAGTA 707
|||||
Db 601 GACCACCTCTTGTATATACACCGTACTATGTGGTCCAGAAAGTGTGGTCCAGAGAAGTA 660

QY 708 TGACAAGTCTGTGACATGTGGTCCCTGGGTGTTCATCATGTACATCCTGC 757
|||||
Db 661 TGACAAGTCTGTGACATGTGGTCCCTGGGTGTTCATCATGTACATCCTGC 710

RESULT 9
CV804995

LOCUS

DEFINITION

CV804995 756 bp mRNA linear EST 15-NOV-2004
AGENCOURT 36395066 NIH_MGC 280 Homo sapiens cDNA clone

IMAGE:7501093 5', mRNA sequence.

ACCESSION

CV804995

VERSION

CV804995.1 GI:55747961

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 756)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Meri Firpo
cDNA Library Preparation: Express Genomics

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM15866 row: 9 column: 11
High quality sequence stop: 652.
Location/Qualifiers
1. .756
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7501093"
/tissue_type="pluripotent cell line derived from blastocyst inner cell mass"
/lab_host="DH10B"
/clone_lib="NIH_MGC_280"
/note="Organ: Blastocyst; Vector: pExpress-1; Site_1: EcorV; Site_2: NotI; RNA obtained from pluripotent cell line derived from blastocyst inner cell mass (cell line HSF-6, NIH Registry designation UC06. Positive for OCT4 expression by rtPCR, positive for SSEA-3, SSEA-4, Tra-1-81, Tra-1-60 by immunofluorescence. Negative for SSEA-1 by immunofluorescence Passage 62. cDNA was primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGGAGCGCGCCC(T)25-3' and cloned into the EcorV/NotI sites of pExpress-1. Size-selection >1.25 kb resulted in an average insert size of 1.8 kb. This primary library is non-normalized (normalized primary library is NIH_MGC_281) and was constructed by Express Genomics (Frederick, MD). Note: this is a Mammalian Gene Collection library."

ORIGIN

Query Match 59.6%; Score 710; DB 8; Length 756;
Best Local Similarity 100.0%; Pred. No. 5.6e-163;
Matches 710; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 AAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAATGCCCCATC 541
Db 1 AAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAATGCCCCATC 60

QY 542 GGGATGTCAAGCCTGAGAATCTCTTATACCTCCAAAAGGCCCAACGCCATCCTGAAAC 601
Db 61 GGGATGTCAAGCCTGAGAATCTCTTATACCTCCAAAAGGCCCAACGCCATCCTGAAAC 120

QY 602 TCACTGACTTTGGCTTGCCAAGGAAACCCACGACCACAACTCTTTGACCACTCCTTGT 661
Db 121 TCACTGACTTTGGCTTGCCAAGGAAACCCACGACCACAACTCTTTGACCACTCCTTGT 180

QY 662 ATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAATATGACAAAGTCCTGTG 721
Db 181 ATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAATATGACAAAGTCCTGTG 240

QY 722 ACATGTGGTCCCTGGGTGCATCATGTACATCTGCTGTGTGGGTATCCCCCTTCTACT 781
Db 241 ACATGTGGTCCCTGGGTGCATCATGTACATCTGCTGTGTGGGTATCCCCCTTCTACT 300

QY 782 CCAACCAAGCCCTTGCCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCCAGTATG 841
Db 301 CCAACCAAGCCCTTGCCATCTCTCCGGGATGAAGACTCGCATCCGAATGGGCCAGTATG 360

QY 842 AATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAATC 901
Db 361 AATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAATC 420

QY 902 TGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGA 961
Db 421 TGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGA 480

QY 962 TCATGCAATCAACAAAGGTCCTCAAACCCCACTGCACACCAAGCCGGTCTCTGAAGGAGG 1021
Db 481 TCATGCAATCAACAAAGGTCCTCAAACCCCACTGCACACCAAGCCGGTCTCTGAAGGAGG 540

QY 1022 ACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCAGTGCCCTTGCCACAATGCGCG 1081
Db 541 ACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCAGTGCCCTTGCCACAATGCGCG 600

QY 1082 TTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACCTCTGCTGCTGA 1141
Db 601 TTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACCTCTGCTGCTGA 660

QY 1142 AGAGGCGGAAGAAAGCTCGGGCCCTGGAGCTCGGCTCTGGCCCCACTGA 1191
Db 661 AGAGGCGGAAGAAAGCTCGGGCCCTGGAGCTCGGCTCTGGCCCCACTGA 710

RESULT 10
BG779875

LOCUS 602667370F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4807072 5', linear EST 15-MAY-2001

DEFINITION mRNA sequence.

ACCESSION BG779875

VERSION BG779875.1 GI:14050192

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 720)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DFP
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM1657 row: 1 column: 17
High quality sequence stop: 719.
Location/Qualifiers
1. .720
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4807072"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_60"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgctcgcc); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 57.8%; Score 688; DB 2; Length 720;
Best Local Similarity 99.0%; Pred. No. 1.4e-157;
Matches 713; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 343 CGGATCGTGGATGTGTACGAGAAATCTGTACGAGGAGGAAGTGCCTGATTGTCATG 402
Db 1 CGGATCGTGGATGTGTACGAGAAATCTGTACGAGGAGGAAGTGCCTGATTGTCATG 60

QY c 1138 CTGAAGAGCGGGAAGAAAGCTCGGGCCCTGGAGGCTGGCGTCTGGCCCACTGA 1191
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Db 722 CTGAAGAGCGGGAAGAAAGCCGGGCCCTGGAGCGCGGCCCTTGCTCACTGA 775
|||||
RESULT 12
AY410231 780 bp DNA linear GSS 16-DEC-2003
LOCUS Mus musculus MAPKAPK2 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY410231
VERSION AY410231.1 GI:39766199
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 780)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 780)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES Location/Qualifiers
source 1..780
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
gene <1..>780
/gene="MAPKAPK2"
/locus_tag="HCM3821"
ORIGIN
Query Match 55.7%; Score 663.2; DB 14; Length 780;
Best Local Similarity 90.6%; Pred. No. 1.7e-151;
Matches 707; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 268 ATGCTTCAGGACTGCCCAAGGCCCGCAGGAGGTGGAGCTGCACCTGGCGGCCTCCCAG 327
|||||
Db 1 ATGCTCCAGGACTGTCCGAAGGCGCGCAGAGAGGTGGAGCTGCACCTGGAGGCCTCCCAG 60
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QY 328 TGCCCGCACATCGTACGGATCGTGGATGTGTACGAGAATCTGTACGAGGAGGAAGTGC 387
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Db 61 TGCCACACATTGTGCACATCGTGGATGTCTATGAGAACCTGTATGCCGGGAGGAAGTGC 120
|||||
QY 388 CTGCTGATTGTCATGGAATGTTTGGACGGTGGAGAACTCTTTAGCCGAATCCAGGATCGA 447
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Db 121 CTGCTGATTGTCATGGAGTGTCTCGATGGTGGAGAGCTCTTTAGTCGAATCCAGGACCGA 180
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QY 448 GGAGACCAGGATTCACAGAAAGAGAACATCCGAAATCATGAAGAGCATCGGTGAGGCC 507
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Db 181 GGAGACCAGGATTCACAGAAAGAGAGGCGTCAGAGATCATGAAGAGCATCGGCGAGGCC 240
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QY 508 ATCCAGTATCTGGATTCAATCAACATTGCCCATCGGGATGTCAAGCTGAGAATCTCTTA 567
|||||
Db 241 ATCCAGTACCTGCACTCGATCAACATTGCTCACCGGGATGTCAAGCCTGAGAACCTCTTA 300
|||||
QY 568 TACACCTCCAAAAGGCCCAACGCCATCCTGAAACTCACTGACTTTGGCTTTGCCAAGGAA 627
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Db 301 TATACTTCCAAAAGGCCCAATGCCAATTTTGAAAACTCACTGATTTTGGCTTTGCCAAGGAA 360
628 ACCACCAGCCCAAACTCTTTGACCACTCCTTGTTATACACCGTACTATGTGGCTCCAGAA 687
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Db 361 ACCACCAGTCACAACTCTTTGACCACTCCGTGTTATACACCATACTATGTGGCTCCGAA 420
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QY 688 GTGCTGGGTCAGAGAAAGTATGACAAGTCCTGTGACATGTGGTCCCTGGGTGTCATCATG 747
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Db 421 GTCTGGGCCGAGAAAGTATGACAAGTCCTGTGACATGTGGTCTTGGGTGTCATCATG 480
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QY 748 TACATCCTGCTGTGTGGGTATCCCCCCTTCTACTCCAACACCGGCCTTGCCCATCTCTCCG 807
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QY 808 GGCATGAAGACTCGCATCCGAATGGGCCAGTATGAATTTCCCAACCCAGAAATGGTCAGAA 867
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Db 541 GGCATGAAGACTCGTATTCGAATGGGCCAGTATGAATTTCTTAACCCGGAGTGGTCAGAA 600
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QY 868 GTATCAGAGGAAGTGAAGATGCTCATTCGGAATCTGCTGAAAAACAGAGCCCACCCAGAGA 927
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Db 601 GTATCAGAGGAAGTGAAGATGCTTATCCGGAATCTGCTAAAAACAGAGCCCACCCAGAGA 660
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QY 928 ATGACCATCACCGAGTTTATGAACCAACCCCTTGGATCATGCAATCAACAAGGTCCCTCAA 987
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Db 661 ATGACCATCACAGAAATTCATGAACCAACCCCTGGATCATGCAATCTACGAAGGTCCCTCAG 720
|||||
QY 988 ACCCCACTGCACACCAGCCGGTCTCTGAAGGAGGACAAGGAGCGGTGGGAGGATGTCAAG 1047
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Db 721 ACTCCACTGCACACCAGCCGTGTCTCTGAAGGAGGACAAGGAACGATGGGAGGATGTCAAG 780
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RESULT 13
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LOCUS AGENCOURT 27272891 NIH MGC 212 Homo sapiens cDNA clone
DEFINITION IMAGE:30925363 5', mRNA sequence.
ACCESSION CO399284
VERSION CO399284.1 GI:49581200
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 855)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mary Hendrix
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM1169 row: e column: 20
High quality sequence stop: 712.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30925363"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH MGC 212"
/note="Organ: Lung; Vector: pYX-Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according

||||| 480 TACACCGTACTATGTGGCTCCAGAAAGTGCTGGGTCCAGAGAAGTATGACAAAGTCTGTGA 539

||||| 723 CATGTGGTCCC-TGGGTGTCATCATGTACATCCTGCTGTGTGGGTATCCCCCCTTCTACT 781

||||| 540 CATGTGGTCCCTTGGGTGTCATCATGTACATCCTGCTGTGTGGGTAT-CCCCATTCTACT 598

||||| 782 CCAACACAGCGCTTGCCATCTCTCCGGGCATGAAGACTCGC----ATCCGAATGGGCCAG 837

||||| 599 CCAACACAGAGCTTG-CATCTCTCCGGGCCTTGACAGACTCGGCATCCTGAATGGGACAG 657

||||| 838 TATGAATTTCCCAACCCAGAAATGGTTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGG 897

||||| 658 TATGACTTTCCCAACCCAGCATGGTTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATACGG 717

||||| 898 AA-TCTGTGAAAAACAGAGCCACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCC 956

||||| 718 AATTCTGCTGAAAAACAGGAGCCCAACAGAGAAATGACCATAACGCAGGTTATGAACCACT 777

||||| 957 TTGGATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCAGCCGGTCTCTGAA 1016

||||| 778 TGGATCTGGAA--TCACAAAGGTCTCTCAAACCCATGGGACACCAAGCGGACCTGACG 834

||||| 1017 GGAGGACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAG 1061

||||| 835 GAGGCCACAGCACGGGCGGAAGAGATGCACAGGACGAGAATAG 879

RESULT 15
BU609266
LOCUS
DEFINITION UI-M-FRO-cap-j-12-0-UI.r1 NIH_BMAP_FRO Mus musculus cDNA clone
IMAGE:6415595 5', mRNA sequence.
ACCESSION BU609266
VERSION BU609266.1 GI:23275481
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 776)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pyX-5.
Location/Qualifiers
1. .776
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6415595"
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/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FRO"
/note="Organ: Brain; Vector: pyX- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 54.8%; Score 652.2; DB 3; Length 776;
Best Local Similarity 91.4%; Pred. No. 8.7e-149;
Matches 701; Conservative 0; Mismatches 65; Indels 1; Gaps 1;
QY 374 CAGGGAGGAAGTGCCTGCTGATTGTTCATGGAAATGTTTGA-CGGTGGAGAACTCTTTAGC 432
Db ||||| 9 CNGGGAGGAAGTGCCTGCTGATTGTTCATGGAGTGTCTCGATNGGTGGAGCTCTTTAGT 68
QY 433 CGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAAGAGAGCATCCGAAATCATGAAG 492
Db ||||| 69 CGAATCCAGGACCGAGGAGACCAGGCATTTCACAGAAAAGAGAGCGTTCAGAGATCATGAAG 128
QY 493 AGCATCGGTAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCATCGGGATGTCAAG 552
Db ||||| 129 AGCATCGGCGAGGCCATCCAGTACCTGCATCGATCAACATTGCTCACCGGGATGTCAAG 188
QY 553 CCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAAACCTCACTGACTTT 612
Db ||||| 189 CCTGAGAACTCTTATATATACTTCCAAAAGGCCCAATGCCATTTTGAACCTCACTGATTTT 248
QY 613 GGCTTTGCCAAGAAACCAACCAGCCACAACACTCTTTGACCACTCCTTGTGTATACACCGTAC 672
Db ||||| 249 GGCTTTGCCAAGAAACCAACCAGTCAACACTCTTTGACCACTCCTCGTGTATACACCATAC 308
QY 673 TATGTGGCTCCAGAAAGTGTGGGTCCAGAGAAGTATGACAAGTCTCTGTGACATGTGGTCC 732
Db ||||| 309 TATGTGGCTCCGAAAGTCTCTGGGCCCGGAGAAAGTATGACAAGTCTCTGTGACATGTGGTCC 368
QY 733 CTGGGTGTCATCATGTACATCCTGTGTGTGGGTATCCCCCCTTCTACTCCAAACCAACGGC 792
Db ||||| 369 TTGGGTGTCATCATGTATATTTTGTGTGTGGGTATCCCCCCTTCTATTCCAATCACGGC 428
QY 793 CTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTATGAATTTCCCAAC 852
Db ||||| 429 CTTGCCATCTCTCCGGGCATGAAGACTCGTATTCGAATGGGCCAGTATGAATTTCCCTAAC 488
QY 853 CCAGAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAATCTGCTGAAAACA 912
Db ||||| 489 CCGGAGTGGTCAGAAAGTATCAGAGAAGTGAAGATGCTTATCCGGAATCTGCTAAAACA 548
QY 913 GAGCCCAACCAGAGAATGACCATCACCGAGTTTATGAACCAACCCCTTGGATCATGCAATCA 972
Db ||||| 549 GAGCCCAACCAGAGAATGACCATCACAGAAATTCATGAACCAACCCCTTGGATCATGCAATCT 608
QY 973 ACAAAGGTCCCTCAAACCCCACTGCAACAGCCGGGTCTCTGAAGGAGGACAAGGAGCGG 1032
Db ||||| 609 ACGAAGGTCCCTCAGACTCCACTGCACACAGCCCGTGTCTCTGAAGGAGGACAAGGAAACGA 668
QY 1033 TGGGAGGATGTCAAGGAGGAGATGACCAGTGCCTTGGCCACAATGCGGCTTGACTACGAG 1092
Db ||||| 669 TGGGAGGATGTCAAGGAGGAGATGACCAGTGCCTTGGCCACGATGCGTGTGACTATGAG 728
QY 1093 CAGATCAAGATAAAAAAGATTGAAGATGCAATCCAAACCCCTCTGCTGCT 1139
Db ||||| 729 CAGATCAAGATAAAGAAGATAGAAGACGCGCATCCAACCCCTCTGCTTCT 775

Search completed: June 19, 2006, 18:05:58
Job time : 6438 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2006, 15:50:24 ; Search time 7102 Seconds
(without alignments)
10723.934 Million cell updates/sec

Title: US-10-469-221-1
Perfect score: 1191
Sequence: 1 tcccaggccagagcccgcc.....ctgcggctctgcccactga 1191

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :		GenEmbl:*	
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		2: gb_pat:*	
		3: gb_ph:*	
		4: gb_pl:*	
		5: gb_pr:*	
		6: gb_ro:*	
		7: gb_sts:*	
		8: gb_sy:*	
		9: gb_un:*	
		10: gb_vi:*	
		11: gb_ov:*	
		12: gb_htg:*	
		13: gb_in:*	
		14: gb_om:*	
		15: gb_ba:*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB ID	Description
		Match	Length		
1	1191	100.0	2974	5	BC052584 Homo sapi
2	1189.4	99.9	1690	5	BC036060 Homo sapi
3	1181.4	99.2	1336	2	AR380852 Sequence
4	1181.4	99.2	1336	5	X75346 H. sapiens m
5	1048.4	88.0	2258	2	AR270852 Sequence
6	1048.4	88.0	2258	2	AX335055 Sequence
7	1048.4	88.0	2258	5	HSU12779 Human MAP k
8	982	82.5	1305	2	DD182194 Methods a
9	967.4	81.2	1065	8	AY335730 Synthetic
10	930	78.1	2909	6	AY197741 Rattus no
11	928.4	78.0	2586	6	BC063064 Mus muscu
12	928.4	78.0	2862	6	BC062048 Rattus no
13	926.8	77.8	2604	6	BC052206 Mus muscu
14	923	77.5	1247	6	MMAPKAP
15	836.4	70.2	1168	2	CS214061 Sequence
16	836.4	70.2	1168	6	CLMAPKAP
17	657.6	55.2	3265	11	BC054572 Danio rer
18	656.6	55.1	768	14	OCMAPKAP

19	656.2	55.1	2786	11	CR761979	CR761979 Xenopus t
20	637.6	53.5	2503	11	BC084300	BC084300 Xenopus l
21	637.6	53.5	2977	11	BC070986	BC070986 Xenopus l
22	563.6	47.3	2654	14	BC103321	BC103321 Bos tauru
23	555.8	46.7	1149	8	AY335561	AY335561 Synthetic
24	555.8	46.7	1149	8	AY892450	AY892450 Synthetic
25	555.8	46.7	1149	8	AY892451	AY892451 Synthetic
26	555.8	46.7	1149	8	BT008118	BT008118 Synthetic
27	555.8	46.7	1298	5	HSU43784	U43784 Human mitog
28	555.8	46.7	2481	2	AR270525	AR270525 Sequence
29	555.8	46.7	2481	5	HSU09578	U09578 Homo sapien
30	555.8	46.7	2494	5	BC007591	BC007591 Homo sapi
31	555.8	46.7	2519	5	BC001662	BC001662 Homo sapi
32	555.8	46.7	2523	5	BC010407	BC010407 Homo sapi
33	546.6	45.9	2634	6	BC081974	BC081974 Rattus no
34	544.6	45.7	2856	6	BC031467	BC031467 Mus muscu
35	533.8	44.8	2484	2	CQ716382	CQ716382 Sequence
36	528	44.3	1333	2	AR145880	AR145880 Sequence
37	476	40.0	1952	6	BC024559	BC024559 Mus muscu
38	448.2	37.6	1982	13	DMU20757	U20757 Drosophila
39	448.2	37.6	2000	2	CQ577905	CQ577905 Sequence
40	448.2	37.6	2025	2	CQ601278	CQ601278 Sequence
41	404	33.9	2049	13	D82877	D82877 Hemacentrot
42	391.6	32.9	1544	13	DQ307182	DQ307182 Glossina
43	366	30.7	600	2	CS217703	CS217703 Sequence
44	269.2	22.6	195485	5	AL591846	AL591846 Human DNA
45	238.4	20.0	502	2	CQ922313	CQ922313 Sequence

ALIGNMENTS

RESULT 1	BC052584	2974 bp	mrna	linear	PRI 30-JUN-2004
LOCUS	Homo sapiens mitogen-activated protein kinase-activated protein kinase 2, transcript variant 2, mRNA (cDNA clone MGC:59706 IMAGE:6267183), complete cds.				
DEFINITION	Homo sapiens mitogen-activated protein kinase-activated protein kinase 2, transcript variant 2, mRNA (cDNA clone MGC:59706 IMAGE:6267183), complete cds.				
ACCESSION	BC052584				
VERSION	BC052584.1 GI:30851682				
KEYWORDS	MGC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2974)				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 2974)				
AUTHORS	Strausberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-MAY-2003) National Institutes of Health, Mammalian				

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc.mgc@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 47 Row: h Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14589905.

FEATURES

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:59706 IMAGE:6267183"
/tissue_type="Skin, melanoma, melanotic"
/clone_lib="NIH MGC 112"
/lab_host="DH10B-R"
/note="Vector: pOTB7"

gene

1. .2974
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/db_xref="GeneID:9261"
/db_xref="MIM:602006"
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/codon_start=1
/product="mitogen-activated protein kinase-activated protein kinase 2, isoform 2"
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/translation="MLNSQGQSPVPFPAPAPPQPTPALPHPPAQP PPPPQQFP QFHVKSGIQIKKNAIIDDYKVTSQVLGLGINGKVLQIFNKRTOBKFKMLQDCPKAR REVELHWKRSQCPIHIVDVYENLYAGRKCLLI VMECLDGGELFSRIQDRGDOAFTE REASEIMKSIGEAIQYLHSINIAHRDVKPENLLYTSKRPNAILKLTDFGFAKETTSN SLTTPCYTPPYVAPEVLGPEKYDKSCDMWSLGVIMYILLCGYPPFFYSNHGLAISPGMK TRIRMGQVEFPNPWESEVSEVKMLIRNLJKTEPTQRTWITIFMNHPIWMQSTKVPQT PLHTRSRLKEDKERWEDVKEEMTSALATMRVDYEIQIKIKKIEDASNPLLLKRRKKARA LEAALAH"

CDS

100.0%; Score 1191; DB 5; Length 2974;
Best Local Similarity 100.0%; Pred. No. 6.1e-313;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 TCCAGGGCCAGAGCCCGGTGCCGTTCCCGCCCGCCCGCCCGCCCGCCAGCCCCC 60
206 TCCAGGGCCAGAGCCCGGTGCCGTTCCCGCCCGCCCGCCCGCCCGCCAGCCCC 265
61 ACCCCTGCCCTGCCGACCCCCCGGCGCAGCCCGCCCGCCCGCCCGCCAGATTCCCC 120
266 ACCCCTGCCCTGCCGACCCCCCGGCGCAGCCCGCCCGCCCGCCCGCCAGATTCCCC 325

ORIGIN

Query Match 100.0%; Score 1191; DB 5; Length 2974;
Best Local Similarity 100.0%; Pred. No. 6.1e-313;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 TCCAGGGCCAGAGCCCGGTGCCGTTCCCGCCCGCCCGCCCGCCCGCCAGCCCCC 60
206 TCCAGGGCCAGAGCCCGGTGCCGTTCCCGCCCGCCCGCCCGCCCGCCAGCCCC 265
61 ACCCCTGCCCTGCCGACCCCCCGGCGCAGCCCGCCCGCCCGCCCGCCAGATTCCCC 120
266 ACCCCTGCCCTGCCGACCCCCCGGCGCAGCCCGCCCGCCCGCCCGCCAGATTCCCC 325

QY	121	CAGTTCACGTC	CAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG	180
Db	326	CAGTTCACGTC	CAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG	385
QY	181	GTCACGAGCC	AGGTCTCTGGGGCTGGGCATCAACGGGCAAGTTTTCAGATCTTCAACAAG	240
Db	386	GTCACGAGCC	AGGTCTCTGGGGCTGGGCATCAACGGGCAAGTTTTCAGATCTTCAACAAG	445
QY	241	AGGACCCAGG	AGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG	300
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QY	301	GTGGAGCTGC	ACTGGCGGCCTCCAGTGCCTCCGCACATCGTACGGATCGTGGATGTGTAC	360
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QY	361	GAGAATCTGT	ACGCAGGGAGGAGTGCTCTGATTGTTCATGGAATGTTTGGACGGTGA	420
Db	566	GAGAATCTGT	ACGCAGGGAGGAGTGCTCTGATTGTTCATGGAATGTTTGGACGGTGA	625
QY	421	GAACCTCTTT	AGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAAGAGATCC	480
Db	626	GAACCTCTTT	AGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAAGAGATCC	685
QY	481	GAATCATGAA	GAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAACATTGCCCAT	540
Db	686	GAATCATGAA	GAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAACATTGCCCAT	745
QY	541	CGGGATGTCA	AGCCTTGAGAATCTTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA	600
Db	746	CGGGATGTCA	AGCCTTGAGAATCTTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA	805
QY	601	CTCACTGACT	TTGGCTTTGCCAAGGAAACCAACAGCCCAACTCTTTTGACCACTCCTTGT	660
Db	806	CTCACTGACT	TTGGCTTTGCCAAGGAAACCAACAGCCCAACTCTTTTGACCACTCCTTGT	865
QY	661	TATACACCGT	ACTATGTGGTCCAGAAAGTCTGGGTCCAGAGAAAGTATGACAAAGTCTCTGT	720
Db	866	TATACACCGT	ACTATGTGGTCCAGAAAGTCTGGGTCCAGAGAAAGTATGACAAAGTCTCTGT	925
QY	721	GACATGTGGT	CCCTGTGCATGTACATCCTGCTGTGTGGTATCCCCCTTCTAC	780
Db	926	GACATGTGGT	CCCTGTGTGCATGTACATCCTGCTGTGTGGTATCCCCCTTCTAC	985
QY	781	TCCAACCA	CGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT	840
Db	986	TCCAACCA	CGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT	1045
QY	841	GAATTTCCAA	CCCAGAAATGGTCAGAAATATCAGAGGAAAGTGAAGATGCTCATTCGGAAT	900
Db	1046	GAATTTCCAA	CCCAGAAATGGTCAGAAATATCAGAGGAAAGTGAAGATGCTCATTCGGAAT	1105
QY	901	CTGCTGAAAA	CAGAGCCCAACAGAGAAATGACCATCACCGAGTTTATGAACCACTTGG	960
Db	1106	CTGCTGAAAA	CAGAGCCCAACAGAGAAATGACCATCACCGAGTTTATGAACCACTTGG	1165
QY	961	ATCATGCAAT	CAACAAAGGTCCCTCAAAACCCCACTGCACACCAAGCCGGGTCTGAAAGGAG	1020
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QY	1021	GACAAGGAG	CGGTGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTGGCCACAATGCGC	1080
Db	1226	GACAAGGAG	CGGTGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTGGCCACAATGCGC	1285
QY	1081	GTTGACTACG	AGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACTCTGTGCTG	1140
Db	1286	GTTGACTACG	AGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACTCTGTGCTG	1345
QY	1141	AAGAGGCGGA	AGAAAGCTCGGGCCCTGGAGGCTCGGGCTCTGGCCCACTGA	1191
Db	1346	AAGAGGCGGA	AGAAAGCTCGGGCCCTGGAGGCTCGGGCTCTGGCCCACTGA	1396

Db	883	TATACACCGTACTATGTGGCTCCAGAAAGTGCTGGGTCCAGAGAAGTATGACAAGTCTCTGT	942
Qy	721	GACATGTGGTCCCTGGGTGTTCATCATGTACATCTCTGTGTGGGTATCCGCCCTTCTTAC	780
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Qy	781	TCCAAACCACGGCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT	840
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Qy	961	ATCATGCAATCAACAAAGGTCCCTCAAAACCCACTGCACACCGCGGTCTCTGAAGGAG	1020
Db	1183	ATCATGCAATCAACAAAGGTCCCTCAAAACCCACTGCACACCGCGGTCTCTGAAGGAG	1242
Qy	1021	GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCATGCGCTTGGCCACAATGCCG	1080
Db	1243	GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCATGCGCTTGGCCACAATGCCG	1302
Qy	1081	GTTGACTACGAGCAGATCAAGATAAAAAGATTGAAGATGCATCCAAACCTCTGCTGCTG	1140
Db	1303	GTTGACTACGAGCAGATCAAGATAAAAAGATTGAAGATGCATCCAAACCTCTGCTGCTG	1362
Qy	1141	AAGAGGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCACTGA	1191
Db	1363	AAGAGGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCACTGA	1413
RESULT 3			
AR380852			
LOCUS	AR380852	1336 bp	DNA
DEFINITION	Sequence 1397 from patent US 6607879.		
ACCESSION	AR380852		
VERSION	AR380852.1 GI:40088486		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1336)		
TITLE	Cocks,B.G., Stuart,S.G. and Seilhamer,J.J. Compositions for the detection of blood cell and immunological response gene expression		
JOURNAL	Patent: US 6607879-A 1397 19-AUG-2003; Incyte Corporation; Palo Alto, CA		
FEATURES	Location/Qualifiers		
source	1..1336 /organism="unknown" /mol_type="genomic DNA"		
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Qy	61	ACCCCTGCCCTGCCGACCCCCCGGGCGAGCCGCGCGCCCGCCCGCCCGAGCTTCCCG	120
Db	61	ACCCCTGCCCTGCCGACCCCCCGGGCGAGCCGCGCGCCCGCCCGCCCGAGCTTCCCG	120
Qy	121	CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAAGACGCCATCATCGATGACTACAAG	180
Db	121	CAGTTCACGTCAGTCCGGCCTGCAGATCAAGAAAGACGCCATCATCGATGACTACAAG	180


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Db |||||||
QY 541 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 600
Db |||||||
QY 931 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 990
QY 601 CTCACTGACTTTGGCTTTGCCAAGGAAACACCAAGGCACAACTCTTTGACCACTCCTTGT 660
Db |||||||
QY 991 CTCACTGACTTTGGCTTTGCCAAGGAAACACCAAGGCACAACTCTTTGACCACTCCTTGT 1050
QY 661 TATACACCGTACTATGTGGCTCCAGAAGTCTGGGTCCAGAGAAGTATGACAAGTCTCTGT 720
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QY 1051 TATACACCGTACTATGTGGCTCCAGAAGTCTGGGTCCAGAGAAGTATGACAAGTCTCTGT 1110
QY 721 GACATGTGTCCTGGGTGTCATCATGTACATCCTGCTGTGTGGGTATCCCCCTTCTAC 780
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QY 781 TCCAAACCAAGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
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QY 1291 CTGCTGAAAAACAGAGCCACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCTTGG 1350
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QY 1351 ATCATGCAATCAACAAGGTCCCTCAAAACCCACTGCACACCCAGCCGGGTCTGAAGGAG 1410
QY 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAG 1050
Db |||||||
QY 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGG 1440
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RESULT 7
HSU12779
LOCUS HSU12779 2258 bp mRNA linear PRI 16-AUG-1994
DEFINITION Human MAP kinase activated protein kinase 2 mRNA, complete cds.
ACCESSION U12779
VERSION U12779.1 GI:530089
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 2258)
AUTHORS Zu,Y.L., Wu,F., Gilchrist,A., Ai,Y., Labadia,M.E. and Huang,C.K.
TITLE The primary structure of a human MAP kinase activated protein
kinase 2
JOURNAL Biochem. Biophys. Res. Commun. 200 (2), 1118-1124 (1994)
PUBMED 8179591
REFERENCE 2 (bases 1 to 2258)
AUTHORS Huang,C.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-1994) Chi-Kuang Huang, Pathology, University of
Connecticut Health Center, 263 Farmington Ave., Farmington, CT
06030, USA
FEATURES
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ORIGIN
Query Match 88.0%; Score 1048.4; DB 5; Length 2258;
Best Local Similarity 99.9%; Pred. No. 3.9e-274;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 391 TCCAGGGCCAGAGCCCGCGGTGCCGTTCCTCCCGCCCGCCCGCCCGCCCGCCCGCC 450
QY 61 ACCCTGCTGCTGCGCACCCCGCGCGAGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 120
Db |||||||
QY 451 ACCCTGCTGCTGCGCACCCCGCGCGAGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 510
QY 121 CAGTTCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 180
Db |||||||
QY 511 CAGTTCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 570
QY 181 GTCACCAAGCCAGGTCTTGGGGCTGGGCATCAACGGCAAGATTTTGACAGATCTTCAACAAG 240
Db |||||||
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QY 241 AGGACCAAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 300
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Db |||||||
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QY 1051 TATACACCGTACTATGTGGCTCCAGAAGTCTGGGTCCAGAGAAGTATGACAAGTCTCTGT 1110
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QY 781 TCCAAACCAAGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
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[illegible]

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QY	518	TGCATTCAATCAACATTGCCCCATCGGGATGTCAAGCCTGAGAAATCTTTATACACCTCCA	577
Db	2075	TGCACTCGATCAACATTGCTCACCGGATGTCAAGCCTGAGAACTCTTATATACTTCCA	2016
QY	578	AAAGGCCCAACGGCATCTCTGAAACTCACTGACTTTGGCTTTGCCAAGGAAACCACCAGCC	637
Db	2015	AAAGGCCCAATGCCATTTTGAAACTCACTGATTTTGGCTTTGGCCAAGGAAACCACCAGTC	1956
QY	638	ACAACTCTTTGACCACTCCTTGTATTATACACGTPACTATGTGGTCCAGAAAGTGTGGGTC	697
Db	1955	ACAACTCTTTGACCACTCCGTGTTATACACCATACTATGTGGTCCGGAAGTCTCTGGGC	1896
QY	698	CAGAGAAGTATGACAAAGTCCTGTGACATGTGGTCCCTGGGTGTCATCATGTACATCCTGC	757
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QY	818	CTCGCATCCGAATGGGCCAGTATGAATTTCCAACCCCAGAAATGGTCAGAAATCATCAGAGG	877
Db	1775	CTCGTATTGCAATGGGCCAGTATGAATTTCTAAACCCGGAGTGGTCAGAAATCATCAGAAG	1716
QY	878	AAGTGAAGATGCTCATTCGGAATCTGCTGAAAAACAGAGCCCCACCCAGAGAATGACCATCA	937
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QY	938	CCGAGTTTATGAACCAACCCCTTGGATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGC	997
Db	1655	CAGAA TTCATGAACCAACCCCTTGGATCATGCAATCTACGAAGGTCCCTCAGACTCCACTGC	1596
QY	998	ACACCAGCCGGTCTCTGAAGGAGGACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGA	1057
Db	1595	ACACCAGCCGTGTCTGAAGGAGGACAAGGAACGATGGGAGGATGTCAAGGAGGAGATGA	1536
QY	1058	CCAGTGCCTTGGCCACAATGCGCGTTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAG	1117
Db	1535	CCAGTGCCTTGGTCACGATGCGTGTTGACTATGAGCAGATCAAGATAAAGAATAGAAG	1476
QY	1118	ATGCATCCAACCCCTCTGCTGTAAGAGGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGG	1177
Db	1475	ACGCATCCAACCCCTCTGCTTCTCAAGAGGCGGAAGAAAGCTCGTGTGTGAGGATGCGG	1416
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Db	1415	CTCTCGCCCACTGA	1402

RESULT 14	
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LOCUS	MMAPKAP
DEFINITION	M. musculus mRNA for MAP kinase-activated protein kinase 2.
ACCESSION	X76850
VERSION	X76850.1 GI:1089895
KEYWORDS	MAP kinase activated protein kinase-2.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
	Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 1241)
AUTHORS	Engel, K., Plath, K. and Gaestel, M.
TITLE	The MAP kinase-activated protein kinase 2 contains a proline-rich SH3-binding domain
JOURNAL	FEBS Lett. 336 (1), 143-147 (1993)
PUBMED	8262198

REFERENCE	2	Gaestel, M.
AUTHORS		Direct Submission
TITLE		Submitted (12-JAN-1994) M. Gaestel, Max-Delbrueck-Zentrum fr.
JOURNAL		Molekulare Medizin, AG Stressproteine, R. Rssle Str. 10, 13122 Berlin, FRG
REMARK		Revised by [3]
REFERENCE	3 (bases 1 to 1247)	
AUTHORS		Gaestel, M.
TITLE		Direct Submission
JOURNAL		Submitted (28-NOV-1995) M. Gaestel, Max-Delbrueck-Zentrum fr.
		Molekulare Medizin, AG Stressproteine, R. Rssle Str. 10, 13122 Berlin, FRG
COMMENT		On Nov 30, 1995 this sequence version replaced gi:441502.
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		polyA_signal
ORIGIN		

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QY	157	AACGCCATCATCGATGACTACAAAGGTCACCAGCCAGGTCCTGGGCTGGGCATCAACGGC	216	
Db	124	AACGCCATCACCGACGACTACAAGGTCACCAGCCAAAGTGTCTGGCCTGGGCATCAACGGG	183	
QY	217	AAAGTTTTGCAGATCTTCAACAAGAGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAG	276	
Db	184	AAGTGTCTGCGGATCTTCGACAAGAGAACCCAGCAAAATTCGCCCTAAAGATGCTCCAG	243	
QY	277	GACTGCCCCAAGCCCCGAGGAGGTGGAGCTGCACCTGGCGGGCCTCCCGAGTCCCGCAC	336	
Db	244	GACTGTCCGAAGCGCGCAGAGAGGTGGAGCTGACTTGGAGGGCCTCCCGAGTCCCGCAC	303	
QY	337	ATCGTACGGATCGTGGATGTGTACGAGAACTGTACGCAGGGAGGAGTGCCTGCTGATT	396	
Db	304	ATTGTGCACATCGTGGATGTCTATGAGAACCTGTATGCCGGAGGAGTGCCTGCTGATT	363	
QY	397	GTCATGGAATGTTTGGACGGTGGAGAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAG	456	
Db	364	GTCATGGAGTGTCTCGATGGTGGAGAGCTCTTTAGTCGAATCCAGGACCGAGGAGACCAG	423	
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Db 484 CTGCACCTCGATCAACATGTCTCACCGGATGTCAAGCTGAGAACCTCTTATATACTTCC 543

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Db 964 CACACCAAGCCGTGCTGAAGGAGGACAAGGAACGATGGGAGGATGTCAAGGAGGAGATG 1023

QY 1057 ACCAGTGCCTTGGCCACAATGCGCGTTGACTACGAGCAGATCAAGATAAAAGATTGAA 1116
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Db 1024 ACCAGTGCCTTGGCCACGATGCGTGTGACTATGAGCAGATCAAGATAAAGAGATAGAA 1083

QY 1117 GATGCATCCAACCTCTGCTGTAAGAGGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCG 1176
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Db 1084 GACGCATCCAACCTCTGCTTCTCAAGAGGCGGAAGAAAGCTCGTGTGTGGAGGATGCG 1143

QY 1177 GCTCTGGCCCACTGA 1191
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Db 1144 GCTCTGCCCACTGA 1158

RESULT 15

CS214061

LOCUS CS214061 1168 bp DNA linear PAT 15-DEC-2005

DEFINITION Sequence 3380 from Patent WO2005111246.

ACCESSION CS214061

VERSION CS214061.1 GI:83681911

KEYWORDS

SOURCE Cricetulus longicaudatus (long-tailed hamster)

ORGANISM Cricetulus longicaudatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Cricetidae; Cricetinae; Cricetulus.

REFERENCE 1

AUTHORS Melville,M.W.

TITLE Oligonucleotide arrays to monitor gene expression and methods for making and using same

JOURNAL Patent: WO 2005111246-A 3380 24-NOV-2005;

Wyeth (US)

FEATURES

source Location/Qualifiers

1..1168

/organism="Cricetulus longicaudatus"

/mol_type="unassigned DNA"

ORIGIN

/db_xref="taxon:10030"

Query Match 70.2%; Score 836.4; DB 2; Length 1168;
Best Local Similarity 90.3%; Pred. No. 2.3e-216;
Matches 894; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 202 CTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAGAGGACCCAGGAGAAATTCGCC 261
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QY 262 CTCAAAATGCTTCAGGACTGCCCCAAGCCGCGCAGGAGGTGGAGCTGCACTGGCGGGCC 321
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Db 61 CTGAAGATGCTCCAGGACTGTCCGAAGGCACGACAGAGAGGTGGAGCTGCACTGGAGGGCC 120

QY 322 TCCAGTGCCCGCACATCGTACGGATCGTGGATGTACGAGAAATCTGTACGAGGGAGG 381
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Db 121 TCCAGTGCCCACACATTTGTGGACATTTGGATGTCTATGAGAACCTGTATGCTGGGAGG 180

QY 382 AAGTGCTGCTGATTGTTCATGGAATGTTTGGACGGTGGAGAACTCTTTAGCCGAATCCAG 441
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Db 181 AAGTGCTGCTGATTGTTCATGGAGTGTCTCGATGGTGGAGAGCTCTTTAGTGAATCCAG 240

QY 442 GATCGAGGAGACCAAGGCATTCACAGAAAGAGAGCATCCGAAATCATGAAGAGCATCGGT 501
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Db 241 GACCGAGGAGACCAAGGCATTCACAGAAAGAGAGCGTCAGAAATCATGAAGAGCATTGGT 300

QY 502 GAGGCCATCCAGTATCTGCATTCATCAATCAATCGCATCGGCATCGGGATGTCAAGCCTGAGAAT 561
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Db 301 GAGGCCATCCAGTATTTGCACTCAATCAATCAATGCTCATCGGGATGTCAAGCCTGAGAAC 360

QY 562 CTCTTATACACTCCAAAAGGCCCAACGCCATCTGAAACTCCTGAAACTCAGTCTTGGCTTTGCC 621
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Db 361 CTCTTATATACTTCCAAAAGGCCCAATGCCATCTGAAACTCAGTGAATTTGGCTTTGCC 420

QY 622 AAGGAAACCAACCAAGCCACAACTCTTTGACCACTCCTGTTATACACCGTACTATGGCT 681
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Db 421 AAGGAAACCAACCAAGTCACAACCTCTGACCACTCCGTGTTATACACCACTACTACGTAGCT 480

QY 682 CCAGAAGTGTGGTCCAGAGAAGTATGACAAAGTCTGTGACATGTGTGCTTGGTGTGTC 741
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QY 742 ATCATGTACATCCTGCTGTGTGGGTATCCCCCTTCTACTCCAACCAAGCCCTTGCCATC 801
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Db 541 ATCATGTATATCTGCTATGTGGGTATCCCCCTTCTATTTCCAATCATGGCCTTGCCATC 600

QY 802 TCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTATGAATTTCCCAACCCAGAAATGG 861
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Db 601 TCTCCGGGTATGAAGACACGATATCCGAATGGGACAGTATGAATTTCTTAACCCAGAAATGG 660

QY 862 TCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAATCTGCTGAAAAACAGAGCCCACC 921
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Db 661 TCAGAAGTATCAGAAAGAGTGAAGATGCTTATCCGGAATCTGCTGAAAAACAGAGCCCACC 720

QY 922 CAGAGAATGACCATCACCGAGTTTATGAACCAACCCCTTGATCATGCAATCAACAAAGGTC 981
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Db 721 CAGAGGATGACCATCACAGAATTTCATGAACCAACCCCTGGATCATGCAATCTACGAAGTC 780

QY 982 CCTCAAAACCCCACTGCACACCAGCCGGGTCTGAAGGAGGACAAGGAGCGGTGGGAGGAT 1041
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Db 781 CCTCAGACTCCACTGCACACCAGCCGTGCTCTGAAGGAGGACAAGGAAACGGTGGGAGGAT 840

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||||| ||| ||||||||| ||| ||||||||| ||| ||||||||| ||| |||

Db 841 GTCAAGGAGGAGATGACCAGTGCCTTGGCCACGATGCGTGTGACTATGAGCAGATCAAG 900

QY 1102 ATAAAAAGATTTGAAGATGCATCCAACCTCTGTCTGTGAAGAGCGGAGAAAGCTCGG 1161
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Db 901 ATAAAGAAAGATAGAAGACGCAATCCAACCTCTGTCTTCTGAAGAGCGGAGAAAGCTCGT 960

QY 1162 GGCCTGGAGGCTGCGGCTCTGGCCCACTGA 1191
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Db 961 GCCGTGGAGGCCGAGCCCTTGCCCCACTGA 990

Search completed: June 19, 2006, 18:02:38
Job time : 7105 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 19, 2006, 08:51:36 ; Search time 298 Seconds
(without alignments)
1229.215 Million cell updates/sec

Title: US-10-469-221-2
Perfect score: 2106
Sequence: 1 SQGQSPVPFPAPAPPPQPP.....PLLLKRRKKARALEAALAH 396

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2106	100.0	400	1	P49137 homo sapien
2	2106	100.0	400	2	Q5SY41_HUMAN
3	1931	91.7	386	1	MAPK2_MOUSE
4	1931	91.7	386	2	Q3U2P8_MOUSE
5	1930	91.6	386	2	Q80ZF4_RAT
6	1882	89.4	370	2	Q5SY30_HUMAN
7	1709	81.1	329	1	MAPK2_CRILLO
8	1687	80.1	377	2	Q61RB4_XENLA
9	1661.5	78.9	374	2	Q5XGX7_XENLA
10	1645	78.1	382	2	Q7T2F2_BRARE
11	1536	72.9	330	1	MAPK2_RABIT
12	1468	69.7	340	2	Q4SRA0_TETNG
13	1391	66.0	382	1	MAPK3_HUMAN
14	1371	65.1	384	1	MAPK3_RAT
15	1370	65.1	384	1	MAPK3_BOVIN
16	1361	64.6	384	1	MAPK3_MOUSE
17	1344.5	63.8	418	2	Q4RXU6_TETNG
18	1340	63.6	416	2	Q4SS24_TETNG
19	1266	60.1	353	2	Q2PQP1_GLOMR
20	1243.5	59.0	350	2	Q25108_HEMPU
21	1211.5	57.5	347	2	Q7PZG1_ANOGA
22	1201	57.0	359	1	MAPK2_DROME
23	1060.5	50.4	391	2	Q61A12_CAEBR
24	1046	49.7	443	2	Q9TZ16_CAEBL
25	1035	49.1	366	2	Q965G5_CAEBL
26	953	45.3	181	2	Q8R3U8_MOUSE
27	796.5	37.8	521	2	Q21360_CAEBL
28	788	37.4	520	2	Q61ZD7_CAEBR
29	740	35.1	495	2	Q6DEV6_XENTR
30	738	35.0	471	2	Q3UV25_MOUSE
31	738	35.0	473	1	MAPK5_MOUSE

32	737.5	35.0	363	2	Q7JM88_CAEBL	Q7jm88 caenorhabdi
33	733	34.8	473	1	MAPK5_HUMAN	Q8iw41 homo sapien
34	730	34.7	471	2	Q6DHN7_BRARE	Q6dhn7 brachydanio
35	717	34.0	459	2	Q4RPT6_TETNG	Q4rpt6 tetraodon n
36	714.5	33.9	346	2	Q65ZB7_CAEBL	Q65zb7 caenorhabdi
37	655.5	31.1	238	2	Q65ZB6_CAEBL	Q65zb6 caenorhabdi
38	613	29.1	201	2	Q8T9D6_DROME	Q8t9d6 drosophila
39	566.5	26.9	249	2	Q8QGH1_CHICK	Q8qgh1 gallus gall
40	564	26.8	336	2	Q8I117_CAEBL	Q8i117 caenorhabdi
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45	540	25.6	735	1	KS6A1_HUMAN	Q15418 homo sapien

ALIGNMENTS

RESULT 1
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ID MAPK2_HUMAN STANDARD; PRT; 400 AA.
AC P49137; Q8IYD6;
DT 01-FEB-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-FEB-1996, sequence version 1.
DT 07-MAR-2006, entry version 52.
DE MAP kinase-activated protein kinase 2 (EC 2.7.1.1-) (MAPK-activated
DE protein kinase 2) (MAPKAP kinase 2) (MAPKAPK-2).
GN Name=MAPKAPK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=94235003; PubMed=8179591;
RA Zu Y.-L., Wu F., Gilchrist A., Ai Y., Labadia M.E., Huang C.K.;
RT "The primary structure of a human MAP kinase activated protein kinase
RT 2.";
RL Biochem. Biophys. Res. Commun. 200:1118-1124(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Skin, and Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 5-400.
RX MEDLINE=94107253; PubMed=8280084;
RA Stokoe D., Caudwell B., Cohen P.T.W., Cohen P.;
RT "The substrate specificity and structure of mitogen-activated protein
RT (MAP) kinase-activated protein kinase-2.";
RL Biochem. J. 296:843-849(1993).
RN [4]

RP INTERACTION WITH PHC2.
RX PubMed=15094067; DOI=10.1016/S0014-5793(04)00351-5;
RA Yannoni Y.M., Gaestel M., Lin L.L.;
RT "P66(ShcA) interacts with MAPKAP kinase 2 and regulates its
activity."; FEBS Lett. 564:205-211(2004).
RL
CC -!- FUNCTION: Its physiological substrate seems to be the small heat
CC shock protein (HSP27/HSP25). In vitro can phosphorylate glycogen
CC synthase at Ser-7 and tyrosine hydroxylase (on Ser-19 and Ser-40).
CC This kinase phosphorylates Ser in the peptide sequence, Hyd-X-R-
CC X(2)-S, where Hyd is a large hydrophobic residue (By similarity).
CC -!- ENZYME REGULATION: Seems to be activated by two distinct pathways:
CC the first involves the stimulation of p42/p44 MAPK by growth
CC factors, the second, triggered by stress and heat shock, depends
CC on the activation of MPK2 and upstream MAPKK/MAPKKK.
CC -!- SUBUNIT: Interacts with PHC2.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P49137-1; Sequence=Displayed;
CC Note=Has a nuclear localization signal;
CC Name=2;
CC IsoId=P49137-2; Sequence=VSP_004910;
CC -!- TISSUE SPECIFICITY: Expressed in all tissues examined.
CC -!- PTM: Phosphorylated and activated by MAP kinase.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: U12779; AAA20851.1; -; mRNA.
DR EMBL: BC036060; AAH36060.2; -; mRNA.
DR EMBL: BC052584; AAH52584.1; -; mRNA.
DR EMBL: X75346; CAA53094.1; -; mRNA.
DR PIR: JC2204; JC2204.
DR PIR: S39793; S39793.
DR PDB: 1KWP; X-ray; A/B=1-400.
DR PDB: 1NXK; X-ray; A/B/C/D=1-400.
DR PDB: 1NY3; X-ray; A=1-400.
DR Ensembl; ENSG00000162889; Homo sapiens.
DR HGNC: HGNC:6887; MAPKAPK2.
DR MIM; 602006; Gene.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR GO; GO:0004871; F:signal transducer activity; TAS.
DR GO; GO:0000165; P:MAPKKK cascade; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW 3D-structure; Alternative splicing; ATP-binding; Kinase;
KW Nucleotide-binding; Phosphorylation; Serine/threonine-protein kinase;
KW Transferase.
FT CHAIN 1 400 MAP kinase-activated protein kinase 2.
FT /FTId=PRO_0000086288.
FT DOMAIN 64 325 Protein kinase.
FT NP_BIND 70 78 ATP (By similarity).
FT COMEBIAS 10 40 Pro-rich.
FT COMPBIAS 35 40 Poly-Pro.
FT ACT_SITE 186 186 Proton acceptor.
FT BINDING 93 93 ATP (By similarity).
FT MOD_RES 328 328 Phosphoserine (by autocatalysis) (By
FT similarity).
FT MOD_RES 334 334 Phosphothreonine (by MAPK) (By
FT similarity).
FT VARSPIC 354 400 EEMTSALATMRVDYEQIKIKKIEDASNPLLLKRKKARALE

AAALAH -> GCLHDKNSDQATWLTRL (in isoform
2).
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H -> D (in Ref. 3).
WS -> LV (in Ref. 3).

FT FT 116 116
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FT FT 76 83
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FT FT 338 344
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Query Match 100.0%; Score 2106; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 7.1e-115;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGQSPVPVFPAPAPPQPPTPALPHPPAQPPPPPPQPFQPHVKSGLQIKQVAIIDDYK 60
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Db 5 SQQSPPVPFAPAPPPQPPTPALPHPPAQPPPPPQFPQFHVKSGLQIKKNAIIDDYK 64

QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVY 120

Db 65 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVY 124

QY 121 ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 180

Db 125 ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 184

QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 240

Db 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 244

QY 241 DMWSLGVIMYILLCGYPFFYSNHGLAISPGMKTRIRMGQYEFNPPEWSEVSEVKMLIRN 300

Db 245 DMWSLGVIMYILLCGYPFFYSNHGLAISPGMKTRIRMGQYEFNPPEWSEVSEVKMLIRN 304

QY 301 LLKTEPTQRTMTITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 360

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QY 361 VDYEQIKIKKIEDASNPDLLKRRKKARALEAAALAH 396

Db 365 VDYEQIKIKKIEDASNPDLLKRRKKARALEAAALAH 400

RESULT 2

Q5SY41 HUMAN

ID Q5SY41 HUMAN PRELIMINARY; PRT; 400 AA.

AC Q5SY41;

DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.

DT 10-MAY-2005, sequence version 1.

DT 07-FEB-2006, entry version 11.

DE Mitogen-activated protein kinase-activated protein kinase 2.

GN Name=MAPKAPK2; ORFNames=RP11-343H5.3-001;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Harrison E.;

RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

CC -----

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CC -----

DR EMBL; AL591846; CA113544.1; -; Genomic_DNA.

DR SMR; Q5SY41; 41-357.

DR Ensembl; ENSG00000162889; Homo sapiens.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0000166; F:nucleotide binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR000719; Prot kinase.

DR InterPro; IPR008271; Ser_thr_pkin_AS.

DR InterPro; IPR002290; Ser_thr_pkinase.

DR InterPro; IPR001245; Tyr_pkinase.

DR Pfam; PF00069; Pkinase; 1.

DR SMART; SM00220; S_TKC; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Nucleotide-binding;

KW Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 400 AA; 45568 MW; E4EFFF11CCF288DC CRC64;

Query Match 100.0%; Score 2106; DB 2; Length 400;

Best Local Similarity 100.0%; Pred. No. 7.1e-115;

Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQSPPVPFAPAPPPQPPTPALPHPPAQPPPPPQFPQFHVKSGLQIKKNAIIDDYK 60

Db 5 SQQSPPVPFAPAPPPQPPTPALPHPPAQPPPPPQFPQFHVKSGLQIKKNAIIDDYK 64

QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVY 120

Db 65 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVY 124

QY 121 ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 180

Db 125 ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 184

QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 240

Db 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 244

QY 241 DMWSLGVIMYILLCGYPFFYSNHGLAISPGMKTRIRMGQYEFNPPEWSEVSEVKMLIRN 300

Db 245 DMWSLGVIMYILLCGYPFFYSNHGLAISPGMKTRIRMGQYEFNPPEWSEVSEVKMLIRN 304

QY 301 LLKTEPTQRTMTITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 360

Db 305 LLKTEPTQRTMTITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 364

QY 361 VDYEQIKIKKIEDASNPDLLKRRKKARALEAAALAH 396

Db 365 VDYEQIKIKKIEDASNPDLLKRRKKARALEAAALAH 400

RESULT 3

MAPK2_MOUSE

ID MAPK2_MOUSE STANDARD; PRT; 386 AA.

AC P49138; Q6P561;

DT 01-FEB-1996, integrated into UniProtKB/Swiss-Prot.

DT 04-JAN-2005, sequence version 2.

DT 07-FEB-2006, entry version 47.

DE MAP kinase-activated protein kinase 2 (EC 2.7.1.-) (MAPK-activated protein kinase 2) (MAPKAP kinase 2) (MAPKAPK-2).

GN Name=Mapkapk2; Synonyms=Rps6kcl;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridea; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA] OF 2-386.

RC TISSUE=Lung;

RX MEDLINE=94085571; PubMed=8262198; DOI=10.1016/0014-5793(93)81628-D;

RA Engel K., Plath K., Gaestel M.;

RT "The MAP kinase-activated protein kinase 2 contains a proline-rich SH3-binding domain.";

RL FEBS Lett. 336:143-147(1993).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptonal landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RX PubMed=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RG Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaïdo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaïdo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AK155171; BAE33092.1; -; mRNA.
DR MGI; MGI:109298; Mapkapk2.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; RCA.
DR GO; GO:0048255; P:mRNA stabilization; IMP.
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DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 386 AA; 44050 MW; ED7827641A826BF3 CRC64;

Query Match 91.7%; Score 1931; DB 2; Length 386;
Best Local Similarity 92.9%; Pred. No. 1.1e-104;
Matches 368; Conservative 7; Mismatches 7; Indels 14; Gaps 2;

QY 1 SQGQSPVPFAPAPPPQPPTPALPHPPPAQPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 60
Db 5 SPGQTPPAPFPSPPPP-----APAQPPP-----FPQFHVKSGLQIRKNAITDDYK 50

QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120
Db 51 VTSQVLGLGINGKVLRIFDKRTQOKFALKMLQDCPKARREVELHWRASQCPHIVHVDVY 110

QY 121 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAQTEREASEIMKSIGEAIQYLHSINIAH 180
Db 111 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAQTEREASEIMKSIGEAIQYLHSINIAH 170

QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 240
Db 171 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 230

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Db 231 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPPEWSEVSEVKMLIRN 290

QY 301 LLKTEPTQRMITTEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 360
Db 291 LLKTEPTQRMITTEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 350

QY 361 VDYEQIKIKKIEDASNPLLLKRRKKARALEAAALAH 396
Db 351 VDYEQIKIKKIEDASNPLLLKRRKKARAVEDAALAH 386

RESULT 5
Q80ZF4 RAT PRELIMINARY; PRT; 386 AA.
AC Q80ZF4;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 23.
DE Mitogen-activated protein kinase-activated protein kinase-2
DE (EC 2.7.1.-) (MAP kinase-activated protein kinase 2).
GN Name=Mapkapk2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BN;
RA Vician L.J., Xu G., Liu W., Feldman J.D., Machado H.B.,
RA Herschman H.R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., MCEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Falvey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
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CC -----
DR EMBL; AY197741; AAO34665.1; -; mRNA.
DR EMBL; BC062048; AAH62048.1; -; mRNA.
DR HSSP; P49137; 1NY3.
DR SMR; Q80ZF4; 29-343.
DR Ensembl; ENSRNOG00000004726; Rattus norvegicus.
DR RGD; 631362; Mapkapk2.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
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DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 386 AA; 44036 MW; 66E827641A827502 CRC64;

Query Match 91.6%; Score 1930; DB 2; Length 386;
Best Local Similarity 92.7%; Pred. No. 1.3e-104;
Matches 367; Conservative 8; Mismatches 7; Indels 14; Gaps 2;

QY 1 SQGQSPVPFAPAPPPQPPTPALPHPPPAQPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 60
Db 5 SPGQTPPAPFPSPPPP-----APAQPPP-----FPQFHVKSGLQIRKNAITDDYK 50

QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120
Db 51 VTSQVLGLGINGKVLRIFDKRTQOKFALKMLQDCPKARREVELHWRASQCPHIVHVDVY 110

QY 121 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAQTEREASEIMKSIGEAIQYLHSINIAH 180
Db 111 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAQTEREASEIMKSIGEAIQYLHSINIAH 170

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Db 291 LLKTEPTQRMITTEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 350

QY 361 VDYEQIKIKKIEDASNPLLLKRRKKARALEAAALAH 396
Db 351 VDYEQIKIKKIEDASNPLLLKRRKKARAVEDAALAH 386


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DR EMBL; BC054572; AAH54572.1; -; mRNA.
DR HSSP; P49137; INY3.
DR SMR; Q7T2F2; 21-338.
DR Ensembl; ENSDARG00000002552; Danio rerio.
DR ZFIN; ZDB-GENE-030131-5532; mapkapk2.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKC_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
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QY 263 HGLAISPGMKTRIRMGQYEFPPNPWESEVSEVKMLIRNLLKTEPTQRTMTITEFMNHPWIM 322
Db 248 HGLAISPGMKKRIRMGQYEFPPNPWESEVSEEAQLIRTLKTEPTQRTMTITEFMNHPWIN 307

QY 323 QSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMRVDYEQIKIKKIEDASNPLLLKR 382
Db 308 QSMVEVPQTPLHTSRVLKEEKDTWEDVKEEMTSALATMRVDYEQIKIKRIEDSTNPLLIK 367

QY 383 RKK 385
Db 368 RKK 370

RESULT 11
MAPK2_RABIT STANDARD; PRT; 330 AA.
ID MAPK2_RABIT
AC P49139;
DT 01-FEB-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-FEB-1996, sequence version 1.
DT 07-MAR-2006, entry version 45.
DE MAP kinase-activated protein kinase 2 (EC 2.7.1.-) (MAPK-activated
DE protein kinase 2) (MAPKAP kinase 2) (MAPKAPK-2) (Fragments).
GN Name=MAPKAPK2;
OS Orctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Orctolagus.
```

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OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 1-256.
RC STRAIN=New Zealand white; TISSUE=Skeletal muscle;
RX MEDLINE=94107253; PubMed=8280084;
RA Stokoe D., Caudwell B., Cohen P.T.W., Cohen P.;
RT "The substrate specificity and structure of mitogen-activated protein
RT (MAP) kinase-activated protein kinase-2.";
RL Biochem. J. 296:843-849(1993).
RN [2]
RP CHARACTERIZATION, PARTIAL PROTEIN SEQUENCE, AND PHOSPHORYLATION SITE
RP THR-300.
RC STRAIN=New Zealand white;
RX MEDLINE=93010994; PubMed=1327754;
RA Stokoe D., Campbell D.G., Nakielny S., Hidaka H., Leeevers S.J.,
RA Marshall C., Cohen P.;
RT "MAPKAP kinase-2; a novel protein kinase activated by mitogen-
RT activated protein kinase.";
RL EMBO J. 11:3985-3999(1992).
CC -!- FUNCTION: Its physiological substrate seems to be the small heat
CC shock protein (HSP27/HSP25). In vitro can phosphorylate glycogen
CC synthase at Ser-7 and tyrosine hydroxylase (on Ser-19 and Ser-40).
CC This kinase phosphorylates Ser in the peptide sequence, Hyd-X-R-
CC X(2)-S, where Hyd is a large hydrophobic residue.
CC -!- ENZYME REGULATION: Seems to be activated by two distinct pathways:
CC the first involves the stimulation of p42/p44 MAPK by growth
CC factors, the second, triggered by stress and heat shock, depends
CC on the activation of MPK2 and upstream MAPKK/MAPKKK.
CC -!- PTM: Phosphorylated and activated by MAP kinase.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; X75345; CAA53093.1; -; mRNA.
DR PIR; S39794; S39794.
DR HSSP; P49137; 1KWP.
DR SMR; P49139; 7-306.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Direct protein sequencing; Kinase; Nucleotide-binding;
KW Phosphorylation; Serine/threonine-protein kinase; Transferase.
KW CHAIN <1 >330 MAP kinase-activated protein kinase 2.
FT FTID=PRO 0000086290.
FT DOMAIN 30 291 Protein kinase.
FT NP_BIND 36 44 ATP (By similarity).
FT COMPBIAS 1 6 Poly-Pro.
FT ACT_SITE 152 152 Proton acceptor (By similarity).
FT BINDING 59 59 ATP (By similarity).
FT MOD_RES 300 300 Phosphothreonine (by MAPK).
FT NON_TER 1 1
FT NON_TER 330 330
SQ SEQUENCE 330 AA; 37579 MW; 487618EF3BE04F53 CRC64;

Query Match 72.9%; Score 1536; DB 1; Length 330;
Best Local Similarity 88.8%; Pred. No. 1e-81;
Matches 293; Conservative 3; Mismatches 34; Indels 0; Gaps 0;

QY 31 PPPPPQQFPQFHVKSLQIKKNAIIDYKVTSSQVLGLGINGKVLQIFNKRTQEKFALKM 90
Db 1 PPPPPQQFPQFHVRSGLQIKKNAIIDYKVTSSQVLGLGINGKVLQIFSKKTQEKFALKM 60

QY 91 LQDCPKARREVELHWRASQCPHIVRIVDVYENLYAGRKCLLIIVMECLDGGELFSRIQDRG 150
Db 61 LQDCPKARREVELHWRASQCPHIVRIVDVYENLYAGRKCLLIIVMECLDGGLLFSRIQDRG 120
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SQ	SEQUENCE	384	AA;	43316	MW;	C9D737DDCF8A0C06	CRC64;
	Query Match			65.1%	Score	1370;	DB 1; Length 384;
	Best Local Similarity			70.8%	Pred. No.	5.9e-72;	
	Matches	257;	Conservative	50;	Mismatches	48;	Indels 8; Gaps 2;
Qy	30	QPPPPPPQFPQPHVKSGL-----QIKKNAIIDDYKVTSQVLGLGINGKVLQIFNKRT	82				
Db	9	QGGPAPPSPGVPCGCSAGAPALGRRREPCKYAVTDDYQLSKQVLGLGVNGKVLCEFHRT	68				
Qy	83	QEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVYENLYAGRKCLLIIVMECLDGGEL	142				
Db	69	GQKALKLLYDSPKARQEVDDHHWQASGGPHIVRILDVYENMHHSKRCLLIIMECEGGEL	128				
Qy	143	FSRIQDRGDAQFTREASEIMKSIGEAIQYLHSINIAHRDVKPENLLYTSKRPNAILKLT	202				
Db	129	FSRIOERGDAQFTREAAAEIMRDIGTAIQFLHSRNIAHRDVKPENLLYTSKDKDAVLKLT	188				
Qy	203	DFGFAKETTSNLSLTTPCYTPYYVAPEVLGPBKVDKSCDMWSLGVIMYILLCGYPPFFYSN	262				
Db	189	DFGFAKETT-QNALQTPCYTPYYVAPEVLGPBKVDKSCDMWSLGVIMYILLCGFPPFFYSN	247				
Qy	263	HGLAISPGMKTRIRMGQYEFPNPEWSEVSEEVKMLIRNLLKTEPTQRMTEITFNMHPWIM	322				
Db	248	TGQAISPGMKRRIRLGLQYGFPSPEWSEVSEDAKQLIRLLKTDPTERLTITQFMNHPWIN	307				
Qy	323	QSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMRVDYEQIKIKKIEDASNPLLLKR	382				
Db	308	QSMVVPQTPLHTARVLQEDRDHWDEVKEEMTSALATMRVDYDQVKIKDLKTSNNRLLNKR	367				
Qy	383	RKK	385				
Db	368	RKK	370				

Search completed: June 19, 2006, 08:59:49
Job time : 300 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 19, 2006, 08:55:01 ; Search time 41 Seconds
(without alignments)
929.313 Million cell updates/sec

Title: US-10-469-221-2
Perfect score: 2106
Sequence: 1 SQGSPVPVFPAPAPPPQPP.....PLLLKRRKKARALEAAALAH 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2078	98.7	396	2 S39793	MAPK-activated pro
2	1921	91.2	385	2 S78100	MAPK-activated pro
3	1882	89.4	370	2 JC2204	MAPK-activated pro
4	1709	81.1	329	2 S49490	MAPK-activated pro
5	1391	66.0	382	1 JC6094	MAPK-activated pro
6	1347	64.0	256	2 S39794	MAPK-activated pro
7	1201	57.0	359	2 JC4297	MAPK-activated pro
8	1046	49.7	443	2 T33690	hypothetical prote
9	796.5	37.8	521	2 T23489	hypothetical prote
10	738	35.0	473	2 JC5952	mitogen-activated
11	540	25.6	735	2 I51901	ribosomal protein
12	531.5	25.2	724	1 B32571	ribosomal protein
13	530.5	25.2	735	2 A53300	ribosomal protein
14	515	24.5	752	1 A32571	ribosomal protein
15	514.5	24.4	374	1 S50193	Ca2+/calmodulin-de
16	512.5	24.3	370	1 S57347	Ca2+/calmodulin-de
17	509	24.2	583	2 H84810	probable calcium-d
18	499.5	23.7	490	1 S71776	calcium-dependent
19	493	23.4	610	1 A49082	calcium-dependent
20	490.5	23.3	740	2 T24340	hypothetical prote
21	490.5	23.3	797	2 T23927	hypothetical prote
22	487.5	23.1	339	2 T34519	MAPK-activated pro
23	487.5	23.1	473	1 A53036	Ca2+/calmodulin-de
24	487.5	23.1	502	2 I52637	Ca2+/calmodulin-de
25	486	23.1	474	1 TVRTC4	Ca2+/calmodulin-de
26	486	23.1	633	2 C32571	ribosomal protein
27	486	23.1	740	2 I38556	ribosomal protein
28	484	23.0	573	2 T09940	calcium-dependent
29	484	23.0	608	2 T18445	hypothetical prote

30	484	23.0	733	1 B30001	ribosomal protein
31	483	22.9	469	1 S17656	Ca2+/calmodulin-de
32	476.5	22.6	541	2 F96776	hypothetical prote
33	476.5	22.6	553	1 T02139	calcium-dependent
34	475.5	22.6	733	2 A57459	ribosomal protein
35	474	22.5	348	2 T37321	Ca2+/calmodulin-de
36	471.5	22.4	802	2 T13149	mitogen-and stress
37	470.5	22.3	301	1 A40811	myosin-light-chain
38	467	22.2	545	2 H86322	calcium-dependent
39	466	22.1	540	1 T01989	calcium-dependent
40	465.5	22.1	582	2 E84721	probable calcium-d
41	464	22.0	493	1 S46283	calcium-dependent
42	464	22.0	639	1 T02784	calcium-dependent
43	463	22.0	1150	2 T13824	LK6 protein kinase
44	460	21.8	509	2 B44412	calmodulin-depende
45	457	21.7	310	2 B88640	protein K07A9.2 [i

ALIGNMENTS

RESULT 1

S39793

MAPK-activated protein kinase 2 (EC 2.7.1.1-) - human (fragment)

N;Alternate names: MAPKAP kinase 2; mitogen-activated protein kinase-activated protein k

C;Species: Homo sapiens (man)

C;Date: 07-Oct-1994 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004

C;Accession: S39793

R;Stokoe, D.; Caudwell, B.; Cohen, P.T.W.; Cohen, P.

Biochem. J. 296, 843-849, 1993

A;Title: The substrate specificity and structure of mitogen-activated protein (MAP) kinase

A;Reference number: S39793; MUID:94107253; PMID:8280084

A;Accession: S39793

A;Molecule type: mRNA

A;Residues: 1-396 <STO>

A;Cross-references: UNIPROT:P49137; UNIPARC:UPI000016AD06; EMBL:X75346; NID:g407074; PID:

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k

F;6-36/Region: proline-rich

F;28-36/Region: SH3-binding motif

F;57-321/Domain: protein kinase homology <KIN>

F;66-74/Region: protein kinase ATP-binding motif

F;381-385/Region: nuclear location signal

F;330/Binding site: phosphate (Thr) (covalent) (by MAP kinase) #status predicted

Query Match 98.7%; Score 2078; DB 2; Length 396;

Best Local Similarity 99.2%; Pred. No. 8.3e-84;

Matches 393; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	SQGSPVPVFPAPAPPPQPTPALPHPPAQP	PPPPPPQFPQFHVKSGLQIKKNAIIDYK	60
Db	1	SQGSPVPVFPAPAPPPQPTPALPHPPAQP	PPPPPPQFPQFHVKSGLQIKKNAIIDYK	60
Qy	61	VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY	120	
Db	61	VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPDIVRVDVY	120	
Qy	121	ENLYAGRKCLLI VMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH	180	
Db	121	ENLYAGRKCLLI VMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH	180	
Qy	181	RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTTPCYTPYVAPEVLGPEKYDKSC	240	
Db	181	RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTTPCYTPYVAPEVLGPEKYDKSC	240	
Qy	241	DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRN	300	
Db	241	DMLVLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRN	300	
Qy	301	LLKTEPTQRM TITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR	360	
Db	301	LLKTEPTQRM TITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR	360	

QY 361 VDYEQIKIKKIEDASNP... 396
Db 361 VDYEQIKIKKIEDASNP... 396

RESULT 2
S78100
MAPK-activated protein kinase (EC 2.7.1.1-) 2 - mouse (fragment)
N;Alternate names: MAPKAP kinase 2; mitogen-activated protein kinase
C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C;Accession: S78100; S39472
R;Gaestel, M.
submitted to the EMBL Data Library, November 1995
A;Description: The MAP kinase-activated protein kinase 2 contains a proline-rich SH3-binding domain
A;Reference number: S78100
A;Accession: S78100
A;Molecule type: mRNA
A;Residues: 1-385 <GAE>
A;Cross-references: UNIPROT:P49138; UNIPARC:UPI00000277C0; EMBL:X76850; NID:g1089895; PIR:G1089895
A;Experimental source: lung
A;Note: this is a revision to the sequence from reference S39472
R;Engel, K.; Plath, K.; Gaestel, M.
FEBS Lett. 336, 143-147, 1993
A;Title: The MAP kinase-activated protein kinase 2 contains a proline-rich SH3-binding domain
A;Reference number: S39472; MUID:94085571; PMID:8262198
A;Accession: S39472
A;Molecule type: mRNA
A;Residues: 3-196, 'R', 198-250, 'K', 252-260, 'N', 262-385 <ENG>
A;Cross-references: UNIPARC:UPI000017556E; EMBL:X76850
A;Note: this sequence has been revised in reference S78100
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
F;9-27/Region: proline-rich
F;21-29/Region: SH3-binding motif
F;46-310/Domain: protein kinase homology <KIN>
F;55-63/Region: protein kinase ATP-binding motif
F;370-374/Region: nuclear location signal
F;319/Binding site: phosphate (Thr) (covalent) (by MAP kinase) #status predicted

Query Match 91.2%; Score 1921; DB 2; Length 385;
Best Local Similarity 92.7%; Pred. No. 5.3e-77;
Matches 367; Conservative 7; Mismatches 8; Indels 14; Gaps 2;

QY 1 SQGQSPVPFPAPAPPQPTPALPHPPAQPPPPQFPQFHVKSGLQIKKNAIIDDYK 60
Db 4 SPGQTPAPFPSPPPP-----APAQPPPP----FPQFHVKSGLQIRKNAITDDYK 49

QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVY 120
Db 50 VTSQVLGLGINGKVLRFDKRTQKFALKMLQDCPKARREVELTWRASQCPHIVHIVDVY 109

QY 121 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAFTEREASEIMKSIGEAIQYLHSINIAH 180
Db 110 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAFTEREASEIMKSIGEAIQYLHSINIAH 169

QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTTPCYTPYYVAPEVLGPEKYDKSC 240
Db 170 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTTPCYTPYYVAPEVLGPEKYDKSC 229

QY 241 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPWSEVSEEVKMLIRN 300
Db 230 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPWSEVSEEVKMLIRN 289

QY 301 LLKTEPTQRMITTEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKESALATMR 360
Db 290 LLKTEPTQRMITTEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKESALATMR 349

QY 361 VDYEQIKIKKIEDASNP... 396
Db 361 VDYEQIKIKKIEDASNP... 396

RESULT 3
JC2204
MAPK-activated protein kinase (EC 2.7.1.1-) 2 - human
N;Alternate names: MAPKAP kinase 2
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: JC2204
R;Zu, Y.L.; Wu, F.; Gilchrist, A.; Ai, Y.; Labadia, M.E.; Huang, C.K.
Biochem. Biophys. Res. Commun. 200, 1118-1124, 1994
A;Title: The primary structure of a human map kinase activated protein kinase 2.
A;Reference number: JC2204; MUID:94235003; PMID:8179591
A;Accession: JC2204
A;Molecule type: mRNA
A;Residues: 1-370 <ZUY>
A;Cross-references: UNIPROT:P49137; UNIPARC:UPI000002AEI8; GB:U12779; NID:g530089; PIDN:12779
A;Experimental source: HL-60 cell
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
F;10-40/Region: proline-rich
F;32-40/Region: SH3-binding motif
F;61-325/Domain: protein kinase homology <KIN>
F;70-78/Region: protein kinase ATP-binding motif
F;334/Binding site: phosphate (Thr) (covalent) (by MAP kinase) #status predicted

Query Match 89.4%; Score 1882; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 2.5e-75;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGQSPVPFPAPAPPQPTPALPHPPAQPPPPQFPQFHVKSGLQIKKNAIIDDYK 60
Db 5 SQGQSPVPFPAPAPPQPTPALPHPPAQPPPPQFPQFHVKSGLQIKKNAIIDDYK 64

QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVY 120
Db 65 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVY 124

QY 121 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAFTEREASEIMKSIGEAIQYLHSINIAH 180
Db 125 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAFTEREASEIMKSIGEAIQYLHSINIAH 184

QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTTPCYTPYYVAPEVLGPEKYDKSC 240
Db 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTTPCYTPYYVAPEVLGPEKYDKSC 244

QY 241 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPWSEVSEEVKMLIRN 300
Db 245 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPWSEVSEEVKMLIRN 304

QY 301 LLKTEPTQRMITTEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 349
Db 305 LLKTEPTQRMITTEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 353

RESULT 4
S49490
MAPK-activated protein kinase 2 (EC 2.7.1.1-) - long-tailed hamster (fragment)
N;Alternate names: MAPKAP kinase 2; mitogen-activated protein kinase-activated protein kinase
C;Species: Cricetulus longicaudatus (long-tailed hamster)
C;Date: 20-Feb-1995 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C;Accession: S49490
R;Huot, J.; Lambert, H.; Lavoie, J.N.; Guimond, A.; Houle, F.; Landry, J.
submitted to the EMBL Data Library, October 1994
A;Description: Characterization of p45-54 hsp27 kinase, a stress sensitive kinase which m
A;Reference number: S49490
A;Accession: S49490
A;Molecule type: mRNA
A;Residues: 1-329 <HUO>
A;Cross-references: UNIPROT:P49136; UNIPARC:UPI000012F196; EMBL:X82220; NID:g559434; PIDN:12779
A;Experimental source: ovary
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
F;1-254/Domain: protein kinase homology (fragment) <KIN>
F;314-318/Region: nuclear location signal

Db	385	TQAPLHSVQQLHGKNLVFSDGYVVKETIGVGSYVCKRCVHKATNMEYAVKVID--KS	441
QY	98	RR-----EVELHWRASQCPHIVRIVDVYENLYAGRKCLLIIVMECLDGGELFSRIQDRGDQA	153
Db	442	KRDPSEEIEILLRYGQHPNIITLKDVYDD---GKHVYLVTELMRGSELLDKILRQ--KF	495
QY	154	FTEREASEIMKSIGEAIQYLHSINIAHRDVKPNLLYTSKRPN-AILKLTDFGFAKETTS	212
Db	496	FSEREASFVLHTISKTVEYLHSQGVVHRDLKPSNILYVDESGNPECLRICDFGFAKQLRA	555
QY	213	HNS-LTTPCYTPYVVAPEVLGPEKYDKSCDMWSLGVIMYILLCGYPPFYNSHGLAISP-G	270
Db	556	ENGLLMTPCYTANFVAPEVLKRQYDEGCDIWSLGIILLYTMLAGYTPF--ANGPSDTPPE	613
QY	271	MKTRIRMGQYEFNPPEWSEVSEVKMLIRNLLKTEPTQRMITITEFMNHPWIMQSTKVPQT	330
Db	614	ILTRIGSGKFTLSGGNWNVTSETAKDLVSKMLHVDPHQRLTAKQVLQHPWITQKDKLPQS	673
QY	331	PL-HTSRVLKEDKERWEDVKEEMTSALATMRVDYEQIKIKKIEDASNPLLLKRRKKARAL	389
Db	674	QLSHQDLQL-----VKGAMAAATYSALNSSKPTPQLKPIESS---ILAQRR--VRKL	719
QY	390	EAAAL 394	
Db	720	PSTTL 724	
RESULT 13			
A53300			
ribosomal protein S6 kinase (EC 2.7.--.) II - rat			
C;Species: Rattus norvegicus (Norway rat)			
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004			
C;Accession: A53300			
R;Grove, J.R.; Price, D.J.; Banerjee, P.; Balasubramanyam, A.; Ahmad, M.F.; Avruch, J.			
Biochemistry 32, 7727-7738, 1993			
A;Title: Regulation of an epitope-tagged recombinant Rsk-1 S6 kinase by phorbol ester an			
A;Reference number: A53300; MUID:93349850; PMID:7688567			
A;Accession: A53300			
A;Status: preliminary; translated from GB/EMBL/DDBJ			
A;Molecule type: mRNA			
A;Residues: 1-735 <RES>			
A;Cross-references: UNIPROT:Q63531; UNIPARC:UPI000012DB2D; GB:M99169; NID:g206771; PIDN:			
C;Genetics:			
A;Gene: Rsk-1			
C;Superfamily: ribosomal protein S6 kinase II; protein kinase homology			
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase			
F;60-321/Domain: protein kinase homology <KIN1>			
F;68-76/Region: protein kinase ATP-binding motif			
F;416-675/Domain: protein kinase homology <KIN2>			
F;424-432/Region: protein kinase ATP-binding motif #status atypical			
Query Match 25.2%; Score 530.5; DB 2; Length 735;			
Best Local Similarity 32.7%; Pred. No. 2e-16;			
Matches 139; Conservative 75; Mismatches 140; Indels 71; Gaps 17;			
QY	16	PPQPPTPALP-----HPPAQPPPPPP-----QQFPQF-HVKSGL-----	48
Db	336	PPFKPAVAQPDDTFYDTEFTSRTPRDSPGIPPSAGAHQLFRGFSFVATGLMEDDSKPRA	395
QY	49	-----QIK-KNAIIDDYKVTQSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKA	97
Db	396	TQAPLHSVQQLHGKNLVFSDGYIVKETIGVGSYVCKRCVHKATNMEYAVKVID---KS	452
QY	98	RR-----EVELHWRASQCPHIVRIVDVYENLYAGRKCLLIIVMECLDGGELFSRIQDRGDQA	153
Db	453	KRDPSEEIEILLRYGQHPNIITLKDVYDD---SKHVYLVTELMRGSELLDKILRQ--KF	506
QY	154	FTEREASEIMKSIGEAIQYLHSINIAHRDVKPNLLYTSKRPN-AILKLTDFGFAKETTS	212
Db	507	FSEREASFVLYTISKTVEYLHSQGVVHRDLKPSNILYVDESGNPECLRICDFGFAKQLRA	566
QY	213	HNS-LTTPCYTPYVVAPEVLGPEKYDKSCDMWSLGVIMYILLCGYPPFYNSHGLAISP-G	270

Db	567	ENGLLMTPCYTANFVAPEVLKRQYDEGCDIWSLGVLLYTMLAGYTPF--ANGPSDTPPE	624
QY	271	MKTRIRMGQYEFNPPEWSEVSEVKMLIRNLLKTEPTQRMITITEFMNHPWIMQSTKVPQT	330
Db	625	ILTRISSGKFTLSGGNWNVTSETAKDLVSKMLHVDPHQRLTAKQVLQHPWITQKDKLPQS	684
QY	331	PL-HTSRVLKEDKERWEDVKEEMTSALATMRVDYEQIKIKKIEDASNPLLLKRRKKARAL	389
Db	685	QLSHQDLQL-----VKGMAAATYSALSSSKPTPQLKPIESS---ILAQRR--VRKL	730
QY	390	EAAAL 394	
Db	731	PSTTL 735	
RESULT 14			
A32571			
ribosomal protein S6 kinase II (EC 2.7.1.-) alpha chain homolog - chicken			
C;Species: Gallus gallus (chicken)			
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004			
C;Accession: A32571			
R;Alcorta, D.A.; Crews, C.M.; Sweet, L.J.; Bankston, L.; Jones, S.W.; Erikson, R.L.			
Mol. Cell. Biol. 9, 3850-3859, 1989			
A;Title: Sequence and expression of chicken and mouse rsk: homologs of Xenopus laevis ril			
A;Reference number: A93113; MUID:89384612; PMID:2779569			
A;Accession: A32571			
A;Molecule type: mRNA			
A;Residues: 1-752 <ALC>			
A;Cross-references: UNIPROT:P18652; UNIPARC:UPI000012DB30; GB:M28488; NID:g551555; PIDN:			
C;Superfamily: ribosomal protein S6 kinase II; protein kinase homology			
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase			
F;78-339/Domain: protein kinase homology <KIN1>			
F;86-94/Region: protein kinase ATP-binding motif			
F;433-692/Domain: protein kinase homology <KIN2>			
Query Match 24.5%; Score 515; DB 1; Length 752;			
Best Local Similarity 34.0%; Pred. No. 9.8e-16;			
Matches 124; Conservative 74; Mismatches 129; Indels 38; Gaps 12;			
QY	28	PAQPPPPPPQFPQFHVKSGLQIKKVAIIDDYKVTQSQVLGLGINGKVLQIFNKRTOEKFA	87
Db	412	PAQPPPLHSVVQ--QLH-----GKNIQFSDGYVVKEAIGVGSYVCKRCIHKTTNMEYA	462
QY	88	LKMLQDCPKARR----EVELHWRASQCPHIVRIVDVYENLYAGRKCLLIIVMECLDGGELF	143
Db	463	VKVID---KSKRDPSEEIEILLRYGQHPNIITLKDVYDD---GKYVYLVTELMRGGELL	515
QY	144	SRIQDRGDQAFTEREASEIMKSIGEAIQYLHSINIAHRDVKPNLLYTSKRPN-AILKLT	202
Db	516	DKILRQ--KFFSEREASSVLHTICKTVEYLHSQGVVHRDLKPSNILYVDESGNPESIRIC	573
QY	203	DFGFAKETTSHNS-LTTPCYTPYVVAPEVLGPEKYDKSCDMWSLGVIMYILLCGYPPFYS	261
Db	574	DFGFAKQLRAENGLLMTPCYTANFVAPEVLKRQYDEGCDIWSLGVLLYTMLAGCTPF--	631
QY	262	NHGLAISP-GMKTRIRMGQYEFNPPEWSEVSEVKMLIRNLLKTEPTQRMITITEFMNHPW	320
Db	632	ANGPSDTPPEILLTRIGGKFSVNGGNWDTISDVAKDLVSKMLHVDPHQRLTAKQVLQHPW	691
QY	321	IMQSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMRVDYEQIKIKKIEDASNPLLL	380
Db	692	ITQKDSLFPQSQLNYQDV-----QLVKGAMAAATYSALNSSKPSPLKPIESS---ILA	740
QY	381	KRRKK 385	
Db	741	QRRVK 745	
RESULT 15			
S50193			
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - rat			
N;Alternate names: CamKI			
C;Species: Rattus norvegicus (Norway rat)			

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Db 121 CAGTTCACGTC AAGTCCGGCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 180

Qy 181 GTCACCAAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAAAGTTTTGCAGATCTTCAACAAG 240

Db 181 GTCACCAAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAAAGTTTTGCAGATCTTCAACAAG 240

Qy 241 AGGACCCAGGAGAAATTCGCCCTCAAATGCTTCAGGACTGCCCCCAAGCCCCGAGGGAG 300

Db 241 AGGACCCAGGAGAAATTCGCCCTCAAATGCTTCAGGACTGCCCCCAAGCCCCGAGGGAG 300

Qy 301 GTGGAGCTGCACTGGCGGGCCTCCAGTGCAGGACCCGCACATCGTACGGATCGTGGATGTGTAC 360

Db 301 GTGGAGCTGCACTGGCGGGCCTCCAGTGCAGGACCCGCACATCGTACGGATCGTGGATGTGTAC 360

Qy 361 GAGAAATCTGTACGAGGGAGGAAGTGCCCTGCTGATTTGTCATGGAATGTTTGGACGGTGA 420

Db 361 GAGAAATCTGTACGAGGGAGGAAGTGCCCTGCTGATTTGTCATGGAATGTTTGGACGGTGA 420

Qy 421 GAACTCTTTAGCCGAATCCAGGATCGAGGACCCAGGCATTCACAGAAAGAGAGCATCC 480

Db 421 GAACTCTTTAGCCGAATCCAGGATCGAGGACCCAGGCATTCACAGAAAGAGAGCATCC 480

Qy 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCTCAATCAACATTGCCCAT 540

Db 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCTCAATCAACATTGCCCAT 540

Qy 541 CGGGATGTCAAGCCTGAGAAATCTCTTTATACACCTCCAAAAGGCCCAAGCCCATCCTGAAA 600

Db 541 CGGGATGTCAAGCCTGAGAAATCTCTTTATACACCTCCAAAAGGCCCAAGCCCATCCTGAAA 600

Qy 601 CTCACTGACTTTGGCTTTGCCAAGGAAACCAACAGCCACAACTCTTTGACCACTCCTTGT 660

Db 601 CTCACTGACTTTGGCTTTGCCAAGGAAACCAACAGCCACAACTCTTTGACCACTCCTTGT 660

Qy 661 TATACACCGTACTATGTGGTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCCCTGT 720

Db 661 TATACACCGTACTATGTGGTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCCCTGT 720

Qy 721 GACATGTGGTCCCTGGGTGTCATCATGTACATCCTGCTGTGTGGGTATCCCCCTTCTAC 780

Db 721 GACATGTGGTCCCTGGGTGTCATCATGTACATCCTGCTGTGTGGGTATCCCCCTTCTAC 780

Qy 781 TCCAAACCAACCGGCTTGCCATCTCTCCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840

Db 781 TCCAAACCAACCGGCTTGCCATCTCTCCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840

Qy 841 GAATTTCCCAACCCAGAAATGGTCAGAAATATCAGAGGAAGTGAAGATGCTATTCGGAAT 900

Db 841 GAATTTCCCAACCCAGAAATGGTCAGAAATATCAGAGGAAGTGAAGATGCTATTCGGAAT 900

Qy 901 CTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 960

Db 901 CTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 960

Qy 961 ATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCCAGCCGGTCTGAAGGAG 1020

Db 961 ATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCCAGCCGGTCTGAAGGAG 1020

Qy 1021 GACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTGGCCACAATGCGC 1080

Db 1021 GACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTGGCCACAATGCGC 1080

Qy 1081 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAAACCTCTGCTGCTG 1140

Db 1081 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAAACCTCTGCTGCTG 1140

Qy 1141 AAGAGGCGGAAGAAAGCTCGGGCCCTGGAGGCTGGGGCTCTGGGCCCACTGA 1191

Db 1141 AAGAGGCGGAAGAAAGCTCGGGCCCTGGAGGCTGGGGCTCTGGGCCCACTGA 1191

; Sequence 3, Application US/10469221
; Publication No. US20040170995A1
; GENERAL INFORMATION:
; APPLICANT: LOGRASSO, PHILIP
; APPLICANT: HAWKINS, JULIO
; APPLICANT: LISNOCK, JEAN MARIE
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: A NOVEL HUMAN SIGNAL, TRANSDUCING KINASE-MAPKAP-2; ENCODED
; TITLE OF INVENTION: PROTEINS, CELLS TRANSFORMED THEREWITH AND USES THEREOF
; FILE REFERENCE: 20813P
; CURRENT APPLICATION NUMBER: US/10/469,221
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: PCT/US02/05670
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/272,260
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Human
; US-10-469-221-3

Query Match 100.0%; Score 1191; DB 8; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCAGGGCCAGAGCCCCGGTGGCGCTTCCCGCCCCGGCCCCCGCCGCGAGCCCCCCC 60
Db 13 TCCAGGGCCAGAGCCCCGGTGGCGCTTCCCGCCCCGGCCCCCGCCGCGAGCCCCCCC 72

Qy 61 ACCCTGCGCTGCCGACCCCCCGGCGCAGCCGCCGCCGCCGCCGCCGCCGAGTTCCTCG 120

Db 73 ACCCTGCGCTGCCGACCCCCCGGCGCAGCCGCCGCCGCCGCCGCCGCCGAGTTCCTCG 132

Qy 121 CAGTTCACCGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 180

Db 133 CAGTTCACCGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 192

Qy 181 GTCACCAAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAAAGTTTTGCAGATCTTCAACAAG 240

Db 193 GTCACCAAGCCAGGTCCTGGGGCTGGGCATCAACGGCAAAAGTTTTGCAGATCTTCAACAAG 252

Qy 241 AGGACCCAGGAGAAATTCGCCCTCAAATGCTTCAGGACTGCCCCAAAGCCCCGAGGGAG 300

Db 253 AGGACCCAGGAGAAATTCGCCCTCAAATGCTTCAGGACTGCCCCAAAGCCCCGAGGGAG 312

Qy 301 GTGGAGTGCACGTGGCGGGCCTCCAGTGCCTCCGCACATCGTACGGATCGTGGATGTGTAC 360

Db 313 GTGGAGTGCACGTGGCGGGCCTCCAGTGCCTCCGCACATCGTACGGATCGTGGATGTGTAC 372

Qy 361 GAGAAATCTGTACGCAGGAGGAAGTGCCCTGCTGATTTGTATGGAATGTTTGGACGGTGA 420

Db 373 GAGAAATCTGTACGCAGGAGGAAGTGCCCTGCTGATTTGTATGGAATGTTTGGACGGTGA 432

Qy 421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTCACAGAAAGAGAGCATCC 480

Db 433 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTCACAGAAAGAGAGCATCC 492

Qy 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCTCAATCAACATTGCCCAT 540

Db 493 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCTCAATCAACATTGCCCAT 552

Qy 541 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACCCCATCCTGAAA 600

Db 553 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACCCCATCCTGAAA 612

Qy 601 CTCACTGACTTTGGCTTTGCCAAGGAAACCAACAGCCACAACTCTTTGACCACCTCCTTGT 660

Db 613 CTCACTGACTTTGGCTTTGCCAAGGAAACCAACAGCCACAACTCTTTGACCACCTCCTTGT 672

Qy 661 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGGTCCAGAGAGTATGACAAGTCTCCTGT 720

Db 673 TATACCGTACTATGTGGCTCCAGAAAGTCTGGGTCCAGAGAAATGATGACAAGTCTCTGT 732
QY 721 GACATGTGGTCCCTGGGTGTTCATGTATCATCTGTCTGTGTGGGTATCCCCCTTCTAC 780
Db 733 GACATGTGGTCCCTGGGTGTTCATGTATCATCTGTCTGTGTGGGTATCCCCCTTCTAC 792
QY 781 TCCAAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
Db 793 TCCAAACCACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 852
QY 841 GAAATTTCCCAACCAGAAATGGTTCAGAAATGATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
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QY 901 CTGCTGAAAAACAGAGCCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCACTTGG 960
Db 913 CTGCTGAAAAACAGAGCCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCACTTGG 972
QY 961 ATCATGCAATCAACAAAGGTCCCTCAAAACCCACTGCACACAGCCGGGTCTGAAGGAG 1020
Db 973 ATCATGCAATCAACAAAGGTCCCTCAAAACCCACTGCACACAGCCGGGTCTGAAGGAG 1032
QY 1021 GACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCAAGTGCCCTTGGCCACAATGCC 1080
Db 1033 GACAAGGAGCGGTGGAGGATGTCAAGGAGGAGATGACCAAGTGCCCTTGGCCACAATGCC 1092
QY 1081 GTTGACTACGAGCAGATCAAGATAAAAAAGATGAAGATGCATCCAAACCTCTGCTGCTG 1140
Db 1093 GTTGACTACGAGCAGATCAAGATAAAAAAGATGAAGATGCATCCAAACCTCTGCTGCTG 1152
QY 1141 AAGAGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCACTGA 1191
Db 1153 AAGAGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCACTGA 1203

RESULT 3

US-10-645-190-3
; Sequence 3, Application US/10645190
; Publication No. US20040110710A1
; GENERAL INFORMATION:
; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
; TITLE OF INVENTION: METHODS FOR PREVENTING ISCHEMIC BRAIN INJURY
; FILE REFERENCE: D0299 NP
; CURRENT APPLICATION NUMBER: US/10/645,190
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/405,586
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1726
; TYPE: DNA
; ORGANISM: Human
US-10-645-190-3

Query Match 99.6%; Score 1186.2; DB 8; Length 1726;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1188; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCTCCCGCCCGCCCGCCCGCGCCCGCCCGCC 60
Db 391 TCCCAGGGCCAGAGCCCGCGGTGCCGTTCCTCCCGCCCGCCCGCCCGCCCGCCCGCC 450
QY 61 ACCCTGCTCCCGCACCCCGCGCGAGCCCGCCCGCCCGCCCGCCCGCCCGCGAGTTCCCG 120
Db 451 ACCCTGCTCCCGCACCCCGCGCGAGCCCGCCCGCCCGCCCGCCCGCCCGCGAGTTCCCG 510
QY 121 CAGTTCCACGTCAAGTCCGGCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 180
Db 511 CAGTTCCACGTCAAGTCCGGCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAAG 570
QY 181 GTCACCAGCCAGGTCCTGGGGCTGGGCAATCAACGGCAAGTTTTTGCAGATCTTCAACAAG 240

Db 571 GTCACCAGCCAGGTCTGGGGCTGGGCAATCAACGGCAAGTTTTGCAGATCTTCAACAAG 630
QY 241 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCCAAGGCCCGCAGGGAG 300
Db 631 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCCAAGGCCCGCAGGGAG 690
QY 301 GTGGAGCTGCACTGGCGGGCCTCCAGTGGCCCGCACATCGTACGGATCGTGGATGTGTAC 360
Db 691 GTGGAGCTGCACTGGCGGGCCTCCAGTGGCCCGCACATCGTACGGATCGTGGATGTGTAC 750
QY 361 GAGAATCTGTACGCGAGGAGGAAGTGCCTGCTGATTTGTATGGAATGTTTGGACGGTGA 420
Db 751 GAGAATCTGTACGCGAGGAGGAAGTGCCTGCTGATTTGTATGGAATGTTTGGACGGTGA 810
QY 421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTCACAGAAAGAGAAGCATCC 480
Db 811 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTCACAGAAAGAGAAGCATCC 870
QY 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCATCAACATTGCCCAT 540
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Db 931 CGGGATGTCAAGCCTGAGAAATCTCTATACACCTCCAAAAGGCCCAACGCCCATCCTGAAA 990
QY 601 CTCACCTGACTTTGGCTTTGCCAAGGAACCCAGCCACCAACTCTTTTGACCACTCCTTGT 660
Db 991 CTCACCTGACTTTGGCTTTGCCAAGGAACCCAGCCACCAACTCTTTTGACCACTCCTTGT 1050
QY 661 TATACACCGTACTATGTGGCTCCAGAAAGTCTGGGTCCAGAGAAAGTATGACAAAGTCTGT 720
Db 1051 TATACACCGTACTATGTGGCTCCAGAAAGTCTGGGTCCAGAGAAAGTATGACAAAGTCTGT 1110
QY 721 GACATGTGTCCTGGGTGTATCATGTATCATCTGCTGTGTGGGTATCCCCCTTCTAC 780
Db 1111 GACATGTGTCCTGGGTGTATCATGTATCATCTGCTGTGTGGGTATCCCCCTTCTAC 1170
QY 781 TCCAACCCAGCCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
Db 1171 TCCAACCCAGCCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
QY 841 GAATTTCCCAACCCAGAAATGGTCAAGATATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
Db 1231 GAATTTCCCAACCCAGAAATGGTCAAGATATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
QY 901 CTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCACTTGG 960
Db 1291 CTGCTGAAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCACTTGG 1350
QY 961 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACAGCCGGGTCTGAAAGGAG 1020
Db 1351 ATCATGCAATCAACAAAGGTCCCTCAAAACCCCACTGCACACAGCCGGGTCTGAAAGGAG 1410
QY 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAGTGCTTGGCCACAATGCGC 1080
Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGAGGAGATGACCAGTGCTTGGCCACAATGCGC 1470
QY 1081 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAAACCTCTGCTGCTG 1140
Db 1471 GTTGACTACGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAAACCTCTGCTGCTG 1530
QY 1141 AAGAGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCACTGA 1191
Db 1531 AAGAGCGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCACTGA 1581

RESULT 4

US-10-641-643-1397
; Sequence 1397, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:


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; SEQ ID NO 238
; LENGTH: 2802
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (613)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1800)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-238

Query Match      90.7%; Score 1080.2; DB 3; Length 2802;
Best Local Similarity 98.7%; Pred. No. 3.2e-308;
Matches 1110; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 68 CCTGCCGCACCCCGCGCGCAGCCGCGCGCCGCGCCGCGCCCGCGCAGTTCCTCCCGCAGTTCC 127
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
56 CGCCGGTGCTGTTCCCGCGCCCGCGCGCCGCGCCCGCGCGCGCGCGCAGTTCCTCCCGCAGTTCC 115

QY 128 ACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAGGTCAACCA 187
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
116 ACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCCATCATCGATGACTACAGGTCAACCA 175

QY 188 GCCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAGAGGACCC 247
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
176 GCCAGGTCCTGGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAGAGGACCC 235

QY 248 AGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCAAAGGCCCGCAGGGAGGTGGAGC 307
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
236 AGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCAAAGGCCCGCA-GGAGGTGGAGC 294

QY 308 TGCACCTGGCGGCCCTCCAGTGCCTGCTGATTTGTCATGGAATGTTTGGACGGTGGAGAACTCT 427
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
295 TGCACCTGGCGGCCCTCCAGTGCCTGCTGATTTGTCATGGAATGTTTGGACGGTGGAGAACTCT 414

QY 368 TGTACGCAGGGAGGAAGTGCCTGCTGATTTGTCATGGAATGTTTGGACGGTGGAGAACTCT 427
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
355 TGTACGCAGGGAGGAAGTGCCTGCTGATTTGTCATGGAATGTTTGGACGGTGGAGAACTCT 414

QY 428 TTAGCCGAATCCAGGATCGAGGAGACCAGGCATTCACAGAAAGAGAGCATCCGAAATCA 487
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
415 TTAGCCGAATCCAGGATCGAGGAGACCAGGCATTCACAGAAAGAGAGCATCCGAAATCA 474

QY 488 TGAAGAGCATCGGTGAGGCCATCCAGTATCTGATTTCAATCAACATTTGCCCATCGGGATG 547
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
475 TGAAGAGCATCGGTGAGGCCATCCAGTATCTGATTTCAATCAACATTTGCCCATCGGGATG 534

QY 548 TCAAGCCTGAGAACTCTTTATACACCTCCAAAAGGCCCAACGCCATCTCTGAAACTCACTG 607
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
535 TCAAGCCTGAGAACTCTTTATACACCTCCAAAAGGCCCAACGCCATCTCTGAAACTCACTG 594

QY 608 ACTTTGGCTTTGCCAAGG-AAACCCAGCCAGCCCAAACTCTTTGACCACTCCTTGTATACA 666
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
595 ACTTTGGCTTTGCCAAGGNAACCCAGCCCAAACTCTTTGACCACTCCTTGTATACA 654

QY 667 CCGTACTATGTGGCTCCAGAAGTGTGGGTCCAGAGAAGTATGACAAAGTCTGTGACATG 726
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
655 CCGTACTATGTGGCTCCAGAAGTGTGGGTCCAGAGAAGTATGACAAAGTCTGTGACATG 714

QY 727 TGGTCCCTGGGTGTCATCATGTACATCCTGTGTGGGTATCCCCCTTCTACTCCAAC 786
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
715 TGGTCCCTGGGTGTCATCATGTACATCCTGTGTGGGTATCCCCCTTCTACTCCAAC 774

QY 787 CACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTATGAATTT 846
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
775 CACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTATGAATTT 834

QY 847 CCCAACCCAGAAATGCTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGGAATCTGCTG 906
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
835 CCCAACCCAGAAATGCTCAGAAGTATCAGAGGAAGTGAAGATGCTCATTCGGGAATCTGCTG 894
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QY 907 AAAACAGAGCCACCCAGAGAATGACCATACCGAGTTTATGAACCAACCCTTGGATCATG 966
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
895 AAAACAGAGCCACCCAGAGAATGACCATACCGAGTTTATGAACCAACCCTTGGATCATG 954

QY 967 CAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCAAGCCGGTCTGAAGGAGGACAAG 1026
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
955 CAATCAACAAAGGTCCCTCAAAACCCCACTGCACACCAAGCCGGTCTGAAGGAGGACAAG 1014

QY 1027 GAGCGGTGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTGGCCACAATGCGCGTTGAC 1086
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1015 GAGCGGTGGAGGATGTCAAGGAGGAGATGACCAAGTGCCTTGGCCACAATGCGCGTTGAC 1074

QY 1087 TAGGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACCCCTCTGCTGTAAGAGG 1146
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1075 TAGGAGCAGATCAAGATAAAAAAGATTGAAGATGCATCCAACCCCTCTGCTGTAAGAGG 1134

QY 1147 CGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCCACTGA 1191
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1135 CGGAAGAAAGCTCGGGCCCTGGAGGCTGCGGCTCTGGCCCCACTGA 1179

RESULT 6
US-09-964-824A-261
; Sequence 261, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatures
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 261
; LENGTH: 2258
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-261

Query Match      88.0%; Score 1048.4; DB 3; Length 2258;
Best Local Similarity 99.9%; Pred. No. 7.5e-299;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCAGGGCCAGAGCCCGCGGTGCGGTTCCTCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
391 TCCAGGGCCAGAGCCCGCGGTGCGGTTCCTCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 450

QY 61 ACCCTGCCCTGCCGACACCCCGCGGCGAGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCG 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
451 ACCCTGCCCTGCCGACACCCCGCGGCGAGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCG 510

QY 121 CAGTTCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCATGACTACAAG 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
511 CAGTTCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCATGACTACAAG 570

QY 181 GTCACCAGCCAGGTCTCTGGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAG 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
571 GTCACCAGCCAGGTCTCTGGGGCTGGGCATCAACGGCAAGTTTTCAGATCTTCAACAAG 630

QY 241 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCCAAGGCCCGCAGGGAG 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
631 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCCAAGGCCCGCAGGGAG 690

QY 301 GTGGAGCTGCACTGGCGGGCCCTCCAGTGGCCCGCACATCGTACGGATCGTGGATGTGTAC 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
691 GTGGAGCTGCACTGGCGGGCCCTCCAGTGGCCCGCACATCGTACGGATCGTGGATGTGTAC 750
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QY 361 GAGAATCTGTACGCAGGGAGGAAGTGCCTGCTGATTGTATGTCATGGAATGTTTGGACGGTGGA 420
Db |||||
QY 421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTTCACAGAAAGAGAAGCATCC 480
Db |||||
QY 481 GAAATCATGAAGACCATCGGTGAGGCCATCCAGTATCTGCAATTCATCAACATTGCCCAT 540
Db |||||
QY 541 CGGGATGTCAAGCCTGAGAAATCTCTTATACACCTCCAAAAGGCCAACGCCATCCTGAAA 600
Db |||||
QY 601 CTCACGTACTTTGGCTTTGCCAAGGAATCTCTTATACACCTCCAAAAGGCCAACGCCATCCTTGT 660
Db |||||
QY 661 TATACACCGCTACTATGTGGTCCAGAAAGTGCTGGGTCCAGAGAAGTATGACAAGTCTCTGT 720
Db |||||
QY 721 GACATGTGTCCTCGGTGTCTCATGTATCATCTGCTGTGGGTATCCCCCTTCTAC 780
Db |||||
QY 781 TCCAAACCAACCGCTTGCCTATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
Db |||||
QY 841 GAATTTCCCAACCCAGAAATGGTCAGAAATCAGAGGAAGTGAAGATGCTCATTTCGGAAT 900
Db |||||
QY 901 CTGCTGAAAAACAGAGCCACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCTTGG 960
Db |||||
QY 961 ATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCCAGCCGGTCTGAAAGGAG 1020
Db |||||
QY 1021 GACAAAGGAGCGGTGGAGGATGTCAAGGGAG 1050
Db |||||
QY 1411 GACAAAGGAGCGGTGGAGGATGTCAAGGGG 1440
Db |||||

RESULT 7
US-10-305-720-1415
; Sequence 1415, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1415
; LENGTH: 2258
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g530089
US-10-305-720-1415

Query Match 88.0%; Score 1048.4; DB 7; Length 2258;
Best Local Similarity 99.9%; Pred. No. 7.5e-299;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCCAGGGCCAGAGCCCGCGGTGCGGTTCCCGCCCCCGCCCCCGCGCCGCCCCCCC 60
Db |||||
QY 391 TCCAGGGCCAGAGCCCGCGGTGCGGTTCCCGCCCCCGCCCCCGCGCCGCCCCCCC 450
Db |||||
QY 61 ACCCTGCTGCGGCAACCCCGCGCGCAGCCCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db |||||
QY 121 CAGTTCACAGTCAAGTCCGGCTGCGAGATCAAGAAGAACGCCATCATCGATGACTACAAG 180
Db |||||
QY 511 CAGTTCACAGTCAAGTCCGGCTGCGAGATCAAGAAGAACGCCATCATCGATGACTACAAG 570
Db |||||
QY 181 GTCACCAAGCAGGTCTCGGGCTGGGCATCAACGGCAAGTTTTCAGAGATCTTCAACAAG 240
Db |||||
QY 571 GTCACCAAGCAGGTCTCGGGCTGGGCATCAACGGCAAGTTTTCAGAGATCTTCAACAAG 630
Db |||||
QY 241 AGGACCCAGAGAAATTTCGCCCTCAAAATGCTTCAGGACTGCCCCAAAGCCCGCAGGGAG 300
Db |||||
QY 631 AGGACCCAGAGAAATTTCGCCCTCAAAATGCTTCAGGACTGCCCCAAAGCCCGCAGGGAG 690
Db |||||
QY 301 GTGGAGCTGCACCTGGCGGGCTCCCAAGTCCCGCACATCGTACGGATCGTGGATGTGTAC 360
Db |||||
QY 691 GTGGAGCTGCACCTGGCGGGCTCCCAAGTCCCGCACATCGTACGGATCGTGGATGTGTAC 750
Db |||||
QY 361 GAGAACTGTACGCAGGGAGGAGTGCCTGCTGATTGTTCATGGAATGTTTGGACGGTGA 420
Db |||||
QY 751 GAGAACTGTACGCAGGGAGGAGTGCCTGCTGATTGTTCATGGAATGTTTGGACGGTGA 810
Db |||||
QY 421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTACAGAAAGAGAAGCATCC 480
Db |||||
QY 811 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGCATTACAGAAAGAGAAGCATCC 870
Db |||||
QY 481 GAAATCATGAAGACCATCGGTGAGGCCATCCAGTATCTGCAATTCATCAACATTGCCCAT 540
Db |||||
QY 541 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 600
Db |||||
QY 931 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 990
Db |||||
QY 601 CTCACGTACTTTGGCTTTGCCAAGGAATGCTGAGTCCAGGCCACAACCTCTTTGACCACTCCTTGT 660
Db |||||
QY 991 CTCACGTACTTTGGCTTTGCCAAGGAATGCTGAGTCCAGATCACCGAGTTTATGAACCAACCTTGG 1050
Db |||||
QY 661 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAGTATGACAAGTCTCTGT 720
Db |||||
QY 1051 TATACACCGTACTATGTGGCTCCAGAAAGTGTGGTCCAGAGAAGTATGACAAGTCTCTGT 1110
Db |||||
QY 721 GACATGTGTCCTCGGTGTCTATGTATCATCTGCTGTGGGTATCCCCCTTCTAC 780
Db |||||
QY 1111 GACATGTGTCCTCGGTGTCTATGTATCATCTGCTGTGGGTATCCCCCTTCTAC 1170
Db |||||
QY 781 TCCAAACCAACCGCTTGCCTATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
Db |||||
QY 841 GAATTTCCCAACCCAGAAATGGTCAGAAATCAGAGGAAGTGAAGATGCTCATTTCGGAAT 900
Db |||||
QY 901 CTGCTGAAAAACAGAGCCACCCAGAGAATGACCATCACCGAGTTTATGAACCAACCTTGG 960
Db |||||
QY 961 ATCATGCAATCAACAAAGGTCCCTCAAACCCCACTGCACACCCAGCCGGTCTGAAAGGAG 1020
Db |||||
QY 1021 GACAAAGGAGCGGTGGAGGATGTCAAGGGAG 1050
Db |||||
QY 1411 GACAAAGGAGCGGTGGAGGATGTCAAGGGG 1440
Db |||||

Db	1411	GACAAGGAGCGGTGGGAGGATGTCAAGGGG	1440
RESULT 8			
US-10-843-641A-5564			
; Sequence 5564, Application US/10843641A			
; Publication No. US20050064454A1			
; GENERAL INFORMATION:			
; APPLICANT: Avalon Pharmaceuticals, Inc.			
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using			
; FILE OF INVENTION: Signature Gene Sets			
; FILE REFERENCE: 689290-189			
; CURRENT APPLICATION NUMBER: US/10/843,641A			
; CURRENT FILING DATE: 2004-05-12			
; PRIOR APPLICATION NUMBER: US/09/873,367			
; PRIOR FILING DATE: 2001-06-05			
; PRIOR APPLICATION NUMBER: US/09/954,531			
; PRIOR FILING DATE: 2001-09-18			
; PRIOR APPLICATION NUMBER: US/09/954,456			
; PRIOR FILING DATE: 2001-09-25			
; PRIOR APPLICATION NUMBER: US/09/962,436			
; PRIOR FILING DATE: 2001-09-25			
; PRIOR APPLICATION NUMBER: US/09/962,832			
; PRIOR FILING DATE: 2001-09-25			
; PRIOR APPLICATION NUMBER: US/09/964,824			
; PRIOR FILING DATE: 2001-09-27			
; PRIOR APPLICATION NUMBER: US/09/967,768			
; PRIOR FILING DATE: 2001-09-28			
; PRIOR APPLICATION NUMBER: US/09/968,007			
; PRIOR FILING DATE: 2001-10-02			
; PRIOR APPLICATION NUMBER: US/09/969,347			
; PRIOR FILING DATE: 2001-10-02			
; PRIOR APPLICATION NUMBER: US/09/969,708			
; PRIOR FILING DATE: 2001-10-03			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 8447			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 5564			
; LENGTH: 2258			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-843-641A-5564			
Query Match 88.0%; Score 1048.4; DB 10; Length 2258;			
Best Local Similarity 99.9%; Pred. No. 7.5e-299;			
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1	TCCCAGGCGCAGAGCCCGCGGTTCGGTTCCTCCCGCCCGCGCCCGCGCGCGCGCCCGCC	60
Db	391	TCCCAGGCGCAGAGCCCGCGGTTCGGTTCCTCCCGCCCGCGCCCGCGCGCGCGCCCGCC	450
QY	61	ACCCCTGCCCTGCCGACCCCGCGCGCAGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	120
Db	451	ACCCCTGCCCTGCCGACCCCGCGCGCAGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	510
QY	121	CAGTCCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG	180
Db	511	CAGTCCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG	570
QY	181	GTCACAGCCAGGTCTCTGGGCTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG	240
Db	571	GTCACAGCCAGGTCTCTGGGCTGGGCATCAACGGCAAAAGTTTTCAGATCTTCAACAAG	630
QY	241	AGGACCCAGGAGAAATTCCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG	300
Db	631	AGGACCCAGGAGAAATTCCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG	690
QY	301	GTGGAGCTGCACCTGGCGGGCCTCCAGTGCCTCCCGCACATCGTACGGATCGTGTGTAC	360
Db	691	GTGGAGCTGCACCTGGCGGGCCTCCAGTGCCTCCCGCACATCGTACGGATCGTGTGTAC	750
QY	361	GAGAACTGTACGCAGGGAGGAAGTGCCTGCTGATTGTCTATGGAATGTTTGGACGGTGA	420
Db	751	GAGAACTGTACGCAGGGAGGAAGTGCCTGCTGATTGTCTATGGAATGTTTGGACGGTGA	810
QY	421	GAACTCTTTAGCCCGAATCCAGGATCGAGGAGACCAGGCATTACAGAAAAGAGAAGCATCC	480
Db	811	GAACTCTTTAGCCCGAATCCAGGATCGAGGAGACCAGGCATTACAGAAAAGAGAAGCATCC	870
QY	481	GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT	540
Db	871	GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATTGCCCAT	930
QY	541	CGGGATGTCAAGCCTGAGAAATCTTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA	600
Db	931	CGGGATGTCAAGCCTGAGAAATCTTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA	990
QY	601	CTCACTGACTTTGGCTTTGCCAAGGAAACCCAGCCACAACTCTTTGACCACCTCCTTGT	660
Db	991	CTCACTGACTTTGGCTTTGCCAAGGAAACCCAGCCACAACTCTTTGACCACCTCCTTGT	1050
QY	661	TATACACCGTACTATGTGGCTCCAGAAAGTCTGGGTCCAGAGAAAGTATGACAAAGTCTGT	720
Db	1051	TATACACCGTACTATGTGGCTCCAGAAAGTCTGGGTCCAGAGAAAGTATGACAAAGTCTGT	1110
QY	721	GACATGTGGTCCCTGGGTGTCTATCATGTACATCCTGCTGTGGGTATCCCCCTTCTAC	780
Db	1111	GACATGTGGTCCCTGGGTGTCTATCATGTACATCCTGCTGTGGGTATCCCCCTTCTAC	1170
QY	781	TCCAAACACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT	840
Db	1171	TCCAAACACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT	1230
QY	841	GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT	900
Db	1231	GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT	1290
QY	901	CTGCTGAAAAACAGAGCCCGCCAGCAATGACCATCACCAGTTTATGAACCCCTTGG	960
Db	1291	CTGCTGAAAAACAGAGCCCGCCAGCAATGACCATCACCAGTTTATGAACCCCTTGG	1350
QY	961	ATCATGCAATCAACAAAGGTCCTCAAAACCCCTCAAAACCCCTCAAAACCCCTCAAGGAG	1020
Db	1351	ATCATGCAATCAACAAAGGTCCTCAAAACCCCTCAAAACCCCTCAAGGAG	1410
QY	1021	GACAAGGAGCGGTGGGAGGATGTCAAGGAG	1050
Db	1411	GACAAGGAGCGGTGGGAGGATGTCAAGGGG	1440
RESULT 9			
US-10-081-119-33			
; Sequence 33, Application US/10081119			
; Publication No. US20030045491A1			
; GENERAL INFORMATION:			
; APPLICANT: Reinhard, Christoph			
; APPLICANT: Jefferson, Anne B.			
; APPLICANT: Chan, Vivien W.			
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic			
; TITLE OF INVENTION: Target in Cancer			
; FILE REFERENCE: 16932.002			
; CURRENT APPLICATION NUMBER: US/10/081,119			
; CURRENT FILING DATE: 2002-02-21			
; PRIOR APPLICATION NUMBER: 60/289,813			
; PRIOR FILING DATE: 2001-02-21			
; NUMBER OF SEQ ID NOS: 38			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 33			
; LENGTH: 2263			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (379) ... (1491)			
US-10-081-119-33			

QY 661 TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCCTGT 720
Db 1051 TATACACCGTACTATGTGGCTCCAGAAGTGCTGGGTCCAGAGAAGTATGACAAGTCCTGT 1110
QY 721 GACATGTGGTCCCTGGGTGTTCATCATGTACATCCTGTGTGTGGGTATCCCCCCTTCTAC 780
Db 1111 GACATGTGGTCCCTGGGTGTTCATCATGTACATCCTGTGTGTGGGTATCCCCCCTTCTAC 1170
QY 781 TCCAAACACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
Db 1171 TCCAAACACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
QY 841 GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
Db 1231 GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
QY 901 CTGCTGAAAACAGAGCCCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCCCTTGG 960
Db 1291 CTGCTGAAAACAGAGCCCCACCCAGAGAAATGACCATCACCGAGTTTATGAACCCCTTGG 1350
QY 961 ATCATGCAATCAACAAAGGTCCTCAAAACCCCACTGCACACCGCGGGTCCTGAAGGAG 1020
Db 1351 ATCATGCAATCAACAAAGGTCCTCAAAACCCCACTGCACACCGCGGGTCCTGAAGGAG 1410
QY 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAG 1050
Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGG 1440

RESULT 11

US-10-951-389-33
; Sequence 33, Application US/10951389
; Publication No. US20050058627A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,389
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (379)...(1491)
US-10-951-389-33

Query Match 88.0%; Score 1048.4; DB 10; Length 2263;
Best Local Similarity 99.9%; Pred. No. 7.5e-299;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCAGGGCCAGAGCCCGCGGTGCGGTTCCCCCGCCCGCGCCCGCGCGAGCCCCC 60
Db 391 TCCAGGGCCAGAGCCCGCGGTGCGGTTCCCCCGCCCGCGCCCGCGCGAGCCCCC 450
QY 61 ACCCTGCCCCTGCCGACCCCCCGCGCAGCCCGCCCGCCCGCCCGCAGGTTCCCG 120
Db 451 ACCCTGCCCCTGCCGACCCCCCGCGCAGCCCGCCCGCCCGCCCGCAGGTTCCCG 510
QY 121 CAGTTCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 180
Db 511 CAGTTCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 570

QY 181 GTCACCAGCCAGGTCTTGGGGTGGGCATCAACGGCAAGTTTTGCAGATCTTCAACAAG 240
Db 571 GTCACCAGCCAGGTCTTGGGGTGGGCATCAACGGCAAGTTTTGCAGATCTTCAACAAG 630
QY 241 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 300
Db 631 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCAAGGCCCGCAGGGAG 690
QY 301 GTGGAGCTGCACCTGGCGGGCCTCCCACTGCCCGCACATCGTACGGATCGTGGATGTGTAC 360
Db 691 GTGGAGCTGCACCTGGCGGGCCTCCCACTGCCCGCACATCGTACGGATCGTGGATGTGTAC 750
QY 361 GAGAATCTGTACGCGAGGAGGAAGTGCCTGCTGATTGTCTATGGAATGTTTGGACGGTGA 420
Db 751 GAGAATCTGTACGCGAGGAGGAAGTGCCTGCTGATTGTCTATGGAATGTTTGGACGGTGA 810
QY 421 GAACTCTTAGCCCGAATCCAGGATCGAGGAGACCGGCATTACAGAAAAGAGAAGCATCC 480
Db 811 GAACTCTTAGCCCGAATCCAGGATCGAGGAGACCGGCATTACAGAAAAGAGAAGCATCC 870
QY 481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCTCAATCAACATTGCCCAT 540
Db 871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCTCAATCAACATTGCCCAT 930
QY 541 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACCCCTGAA 600
Db 931 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACCCCTGAA 990
QY 601 CTCACCTGACTTTGGCTTTGCCAAGGAAACCAACGAGCCCAACTCTTTGACCACCTCCTGT 660
Db 991 CTCACCTGACTTTGGCTTTGCCAAGGAAACCAACGAGCCCAACTCTTTGACCACCTCCTGT 1050
QY 661 TATACACCGTACTATGTGGCTCCAGAAGTGTGGTCCAGAGAAGTATGACAAGTCCTGT 720
Db 1051 TATACACCGTACTATGTGGCTCCAGAAGTGTGGTCCAGAGAAGTATGACAAGTCCTGT 1110
QY 721 GACATGTGGTCCCTGGGTGTTCATGTATCATCTCTGTGTGGGTATCCCCCCTTCTAC 780
Db 1111 GACATGTGGTCCCTGGGTGTTCATGTATCATCTCTGTGTGGGTATCCCCCCTTCTAC 1170
QY 781 TCCAAACACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
Db 1171 TCCAAACACGGCCTTGCCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
QY 841 GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
Db 1231 GAATTTCCCAACCCAGAAATGGTCAGAAAGTATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
QY 901 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCCCTTGG 960
Db 1291 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCCCTTGG 1350
QY 961 ATCATGCAATCAACAAAGTTCCTCAAAACCCCACTGCACACCGCGGGTCCTGAAGGAG 1020
Db 1351 ATCATGCAATCAACAAAGTTCCTCAAAACCCCACTGCACACCGCGGGTCCTGAAGGAG 1410
QY 1021 GACAAGGAGCGGTGGGAGGATGTCAAGGAG 1050
Db 1411 GACAAGGAGCGGTGGGAGGATGTCAAGGGG 1440

RESULT 12

US-10-951-406-33
; Sequence 33, Application US/10951406
; Publication No. US20050059630A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,406


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Db      691 GTGGAGCTGCACTGGCGGGCTCCAGTGCCTCCGCACATCGTACGGATCGTGGATGTGTAC 750
QY      361 GAGAAATCTGTACGCAGGGAGGAAGTGCCTGCTGATTGTTCATGGAATGTTTGGACGGTGA 420
Db      751 GAGAAATCTGTACGCAGGGAGGAAGTGCCTGCTGATTGTTCATGGAATGTTTGGACGGTGA 810
QY      421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGATTCACAGAAAGAGAAGCATCC 480
Db      811 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGATTCACAGAAAGAGAAGCATCC 870
QY      481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATGCCCCAT 540
Db      871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATGCCCCAT 930
QY      541 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 600
Db      931 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 990
QY      601 CTCACCTGACTTTGGCTTTGCCAAGGAAACCCAGCCACCACTCTTTTGACCACTCCTTGT 660
Db      991 CTCACCTGACTTTGGCTTTGCCAAGGAAACCCAGCCACCACTCTTTTGACCACTCCTTGT 1050
QY      661 TATACACCGTACTATGTGGCTCCAGAAAGTCTGGGTCCAGAGAAAGTATGACAAATCCTGT 720
Db      1051 TATACACCGTACTATGTGGCTCCAGAAAGTCTGGGTCCAGAGAAAGTATGACAAATCCTGT 1110
QY      721 GACATGTGGTCCCTGGGTGTATCATGTATCATCTCTGTGTGGGTATCCCCCTTCTAC 780
Db      1111 GACATGTGGTCCCTGGGTGTATCATGTATCATCTCTGTGTGGGTATCCCCCTTCTAC 1170
QY      781 TCCAAACCAACGGCTTGCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 840
Db      1171 TCCAAACCAACGGCTTGCATCTCTCCGGGCATGAAGACTCGCATCCGAATGGGCCAGTAT 1230
QY      841 GAATTTCCCAACCCAGAAATGGTCAGAAATATCAGAGGAAGTGAAGATGCTCATTCGGAAT 900
Db      1231 GAATTTCCCAACCCAGAAATGGTCAGAAATATCAGAGGAAGTGAAGATGCTCATTCGGAAT 1290
QY      901 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 960
Db      1291 CTGCTGAAAACAGAGCCCAACCCAGAGAAATGACCATCACCGAGTTTATGAACCAACCTTGG 1350
QY      961 ATCATGCAATCAACAAAGGTCCTCAAACCCCACTGCACACCAGCCGGTCTCTGAAGGAG 1020
Db      1351 ATCATGCAATCAACAAAGGTCCTCAAACCCCACTGCACACCAGCCGGTCTCTGAAGGAG 1410
QY      1021 GACAAGGAGCGGTGGAGGATGTCAAGGAG 1050
Db      1411 GACAAGGAGCGGTGGAGGATGTCAAGGGG 1440
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RESULT 14

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US-10-977-087-33
; Sequence 33, Application US/10977087
; Publication No. US20050130926A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; APPLICANT: Kaufmann, Joerg
; APPLICANT: Xin, Hong
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Khoja, Hamiduddin
; APPLICANT: Shyamala, Venkatakrishna
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS CELLS
; FILE REFERENCE: 2300-21986
; CURRENT APPLICATION NUMBER: US/10/977,087
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: 10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/271,254
```

```
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 10/360,848
; PRIOR FILING DATE: 2003-02-06
; PRIOR APPLICATION NUMBER: 09/570,593
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134,112
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 10/763,692
; PRIOR FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: 09/626,301
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/148,936
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/145,612
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 10/698,959
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (379)...(1491)
US-10-977-087-33
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Query Match      88.0%; Score 1048.4; DB 10; Length 2263;
Best Local Similarity 99.9%; Pred. No. 7.5e-299;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 TCCAGGGCCAGAGCCCGCGGTGCCGTTCCTCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 60
Db      391 TCCAGGGCCAGAGCCCGCGGTGCCGTTCCTCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 450
QY      61 ACCCTGCCCTGCCCGCACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db      451 ACCCTGCCCTGCCCGCACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 510
QY      121 CAGTTCCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 180
Db      511 CAGTTCCACGTCAAGTCCGGCCTGCAGATCAAGAAGAACGCCATCATCGATGACTACAAG 570
QY      181 GTCACAGCAGGTCTCTGGGGTGGGCATCAACGGCAAGTTTTTGAGATCTTCAACAAG 240
Db      571 GTCACAGCAGGTCTCTGGGGTGGGCATCAACGGCAAGTTTTTGAGATCTTCAACAAG 630
QY      241 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCAGGCCCGCAGGGAG 300
Db      631 AGGACCCAGGAGAAATTCGCCCTCAAAATGCTTCAGGACTGCCCCAGGCCCGCAGGGAG 690
QY      301 GTGGAGCTGCACCTGGCGGCCCTCCAGTGCCTCCGCACATCGTACGGATCGTGGATGTGTAC 360
Db      691 GTGGAGCTGCACCTGGCGGCCCTCCAGTGCCTCCGCACATCGTACGGATCGTGGATGTGTAC 750
QY      361 GAGAAATCTGTACGCAGGGAGGAAGTGCCTGCTGATTGTTCATGGAATGTTTGGACGGTGA 420
Db      751 GAGAAATCTGTACGCAGGGAGGAAGTGCCTGCTGATTGTTCATGGAATGTTTGGACGGTGA 810
QY      421 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGATTCACAGAAAGAGAAGCATCC 480
Db      811 GAACTCTTTAGCCGAATCCAGGATCGAGGAGACCAGGATTCACAGAAAGAGAAGCATCC 870
QY      481 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATGCCCCAT 540
Db      871 GAAATCATGAAGAGCATCGGTGAGGCCATCCAGTATCTGCATTCAATCAACATGCCCCAT 930
QY      541 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 600
Db      931 CGGGATGTCAAGCCTGAGAATCTCTTATACACCTCCAAAAGGCCCAACGCCATCCTGAAA 990
```


GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein,search, using sw model
Run on: June 19, 2006, 08:51:16 ; Search time 199 Seconds
(without alignments)
909.838 Million cell updates/sec

Title: US-10-469-221-2
Perfect score: 2106
Sequence: 1 SQGSPVPFPAPAPPQPP.....PLLLKRRKKARALEAAALAH 396

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2106	100.0	396	6	AAE29898	Aae29898 Human tru
2	2106	100.0	400	6	AAE29899	Aae29899 Human ful
3	2106	100.0	400	7	ADC15042	Adc15042 Mitogen a
4	2106	100.0	400	7	ADE58649	Ades58649 Human Pro
5	2106	100.0	400	7	ADN02271	Adn02271 Human MK-
6	2106	100.0	400	8	ADN61583	Adn61583 Human nat
7	2097	99.6	400	8	ADM36340	Adm36340 Human MK2
8	2097	99.6	400	9	ADX06660	Adx06660 Cyclin-de
9	1921	91.2	385	7	ADE60496	Ade60496 Rat Prote
10	1921	91.2	385	7	ADD47657	Add47657 Rat Prote
11	1886	89.6	378	8	ABM82670	Abm82670 Human dia
12	1882	89.4	370	5	ABP54949	Abp54949 Human MAP
13	1882	89.4	370	7	ABU61622	Abu61622 Human can
14	1882	89.4	370	8	ADM36338	Adm36338 Human MK2
15	1882	89.4	370	8	ADP87579	Adp87579 Human NOV
16	1882	89.4	370	9	ADX06658	Adx06658 Cyclin-de
17	1882	89.4	370	9	ADY86798	Ady86798 Human MAP
18	1882	89.4	370	9	AEA89440	Aea89440 Human MAP
19	1882	89.4	375	8	ADP87585	Adp87585 Human NOV
20	1870	88.8	370	8	ADP87583	Adp87583 Human NOV
21	1870	88.8	370	8	ADP87587	Adp87587 Human NOV
22	1828	86.8	357	9	ADY85543	Ady85543 Catalytic
23	1803	85.6	338	8	ADP87589	Adp87589 Human NOV

24	1729	82.1	327	7	ADN02272	Adn02272 Human MK-
25	1729	82.1	434	6	ABR83629	AbR83629 SUMO-MPAK
26	1716	81.5	326	8	ADN61586	Adn61586 Human MAP
27	1596	75.8	324	6	ABR41296	AbR41296 Human DIT
28	1552	73.7	294	8	ADP87591	Adp87591 Human NOV
29	1552	73.7	294	8	ADP87581	Adp87581 Human NOV
30	1391	66.0	382	2	AAW31910	Aaw31910 Human MAP
31	1391	66.0	382	7	ADC15043	Adc15043 Mitogen a
32	1391	66.0	382	7	ADD14163	Add14163 Human src
33	1391	66.0	382	7	ADE60498	Ade60498 Human Pro
34	1391	66.0	382	7	ADD47659	Add47659 Human Pro
35	1391	66.0	382	7	ADN95701	Adn95701 Human BEC
36	1391	66.0	382	8	ADN03900	Adn03900 Antipsori
37	1391	66.0	382	8	ADN61584	Adn61584 Human MAP
38	1391	66.0	382	8	ADO52466	Ado52466 Human BRC
39	1391	66.0	382	8	ABM80460	Abm80460 Tumour-as
40	1391	66.0	382	9	AEEl9659	Aeel9659 Human MAP
41	1391	66.0	383	7	ADD46033	Add46033 Human Pro
42	1381	65.6	382	9	AEEl9663	Aeel9663 Human MAP
43	1379	65.5	382	9	AEEl9665	Aeel9665 Human MAP
44	1261.5	59.9	355	8	ABM83772	Abm83772 Human dia
45	1261.5	59.9	355	8	ABM83774	Abm83774 Human dia

ALIGNMENTS

RESULT 1
AAE29898
ID AAE29898 standard; protein; 396 AA.
XX
AC AAE29898;
XX
DT 24-MAR-2003 (first entry)
XX
DE Human truncated MAPKAP-2 kinase, tdnaMAPKAP-2.
XX
KW Human; mitogen-activated protein kinase activating protein kinase-2;
KW MAPKAP-2 kinase; signal transduction; cell proliferative disorder;
KW immune system disorder; inflammation; arthritis; immunomodulator;
KW cytostatic; gene therapy; enzyme.
XX
OS Homo sapiens.
XX
PN WO200290524-A2.
XX
PD 14-NOV-2002.
XX
PF 25-FEB-2002; 2002WO-US005670.
XX
PR 28-FEB-2001; 2001US-0272260P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Lograsso P, Hawkins J, Lisnock JM;
XX
DR WPI; 2003-111970/10.
DR N-PSDB; AAD50036.
XX
PT New isolated nucleic acid molecule encoding a human mitogen-activated
PT protein kinase activating protein kinase-2 (MAPKAP-2), useful for
PT treating immune-system related disorders, inflammation and arthritis.
XX
PS Claim 11; Fig 2; 150pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule comprising a
CC sequence of nucleotides that encode a human mitogen-activated protein
CC kinase activating protein kinase-2 (MAPKAP-2 kinase) and a coding region
CC that encodes a splice variant of a MAPKAP-2 kinase. The invention is
CC especially useful in regulating signal transduction in a cell and in
CC diagnosing or treating MAPKAP-2-mediated disorders eg. cell proliferative
CC disorders, immune system disorders, inflammation, arthritis. The nucleic
CC acid and the polypeptide may also be used in screening assays, predictive

CC medicine, diagnostic or prognostic assays, chromosome mapping, tissue
CC typing, pharmacogenomics and in monitoring clinical trials. The invention
CC is useful in gene therapy. The present sequence is human truncated MAPKAP
CC -2 kinase, tdnMAPKAP-2
XX
SQ Sequence 396 AA;

Query Match 100.0%; Score 2106; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 2e-161;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQSPPVPFPAPAPPQPTPALPHPPAQP PPPPPQFPQFHVKSGLQIKKNAIIDDYK 60
Db 1 SQQSPPVPFPAPAPPQPTPALPHPPAQP PPPPPQFPQFHVKSGLQIKKNAIIDDYK 60

QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120
Db 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120

QY 121 ENLYAGRKCLLI VMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 180
Db 121 ENLYAGRKCLLI VMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 180

QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 240
Db 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 240

QY 241 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRN 300
Db 241 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRN 300

QY 301 LLKTEPTQRTMITFEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 360
Db 301 LLKTEPTQRTMITFEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 360

QY 361 VDYEQIKIKKIEDASNPLLLKRRKKARALEAAALAH 396
Db 361 VDYEQIKIKKIEDASNPLLLKRRKKARALEAAALAH 396

RESULT 2
AAE29899
ID AAE29899 standard; protein; 400 AA.
XX
AC AAE29899;
XX
DT 24-MAR-2003 (first entry)
XX
DE Human full length MAPKAP-2 kinase, fldnaMAPKAP-2.
XX
KW Human; mitogen-activated protein kinase activating protein kinase-2;
KW MAPKAP-2 kinase; signal transduction; cell proliferative disorder;
KW immune system disorder; inflammation; arthritis; immunomodulator;
KW cytostatic; gene therapy; enzyme.
XX
OS Homo sapiens.
XX
PN WO200290524-A2.
XX
PD 14-NOV-2002.
XX
PF 25-FEB-2002; 2002WO-US005670.
XX
PR 28-FEB-2001; 2001US-0272260P.
XX
XX (MERI) MERCK & CO INC.
XX
XX Lograsso P, Hawkins J, Lisnock JM;
PI
XX WPI; 2003-111970/10.
DR
DR N-PSDB; AAD50037.
XX
PT New isolated nucleic acid molecule encoding a human mitogen-activated

PT protein kinase activating protein kinase-2 (MAPKAP-2), useful for
PT treating immune-system related disorders, inflammation and arthritis.
XX
XX Claim 66; Fig 4; 150pp; English.
PS
XX
CC The invention relates to an isolated nucleic acid molecule comprising a
CC sequence of nucleotides that encode a human mitogen-activated protein
CC kinase activating protein kinase-2 (MAPKAP-2 kinase) and a coding region
CC that encodes a splice variant of a MAPKAP-2 kinase. The invention is
CC especially useful in regulating signal transduction in a cell and in
CC diagnosing or treating MAPKAP-2-mediated disorders eg. cell proliferative
CC disorders, immune system disorders, inflammation, arthritis. The nucleic
CC acid and the polypeptide may also be used in screening assays, predictive
CC medicine, diagnostic or prognostic assays, chromosome mapping, tissue
CC typing, pharmacogenomics and in monitoring clinical trials. The invention
CC is useful in gene therapy. The present sequence is human full length
CC MAPKAP-2 kinase, fldnaMAPKAP-2
XX
SQ Sequence 400 AA;

Query Match 100.0%; Score 2106; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.1e-161;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQQSPPVPFPAPAPPQPTPALPHPPAQP PPPPPQFPQFHVKSGLQIKKNAIIDDYK 60
Db 5 SQQSPPVPFPAPAPPQPTPALPHPPAQP PPPPPQFPQFHVKSGLQIKKNAIIDDYK 64

QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120
Db 65 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 124

QY 121 ENLYAGRKCLLI VMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 180
Db 125 ENLYAGRKCLLI VMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 184

QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 240
Db 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 244

QY 241 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRN 300
Db 245 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRN 304

QY 301 LLKTEPTQRTMITFEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 360
Db 305 LLKTEPTQRTMITFEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVKEEMTSALATMR 364

QY 361 VDYEQIKIKKIEDASNPLLLKRRKKARALEAAALAH 396
Db 365 VDYEQIKIKKIEDASNPLLLKRRKKARALEAAALAH 400

RESULT 3
ADC15042
ID ADC15042 standard; protein; 400 AA.
XX
AC ADC15042;
XX
DT 18-DEC-2003 (first entry)
XX
DE Mitogen activated protein kinase activated protein kinase 2 (MAPKAPK2) .
XX
KW Mitogen activated protein kinase activated protein kinase 2; MAPKAPK2;
KW crystal structure; three dimensional structure; ATP binding pocket;
KW substrate binding pocket; nuclear export signal motif;
KW MAP kinase signal transduction pathway; cellular stress;
KW bacterial lipopolysaccharide; proinflammatory cytokine; TNF-alpha;
KW tumour necrosis factor-alpha; drug screening; rational drug design;
KW protein co-ordinate data; enzyme.
XX
OS Unidentified.
XX

FH Key Location/Qualifiers
FT Binding-site 77..78 /note= "These residues are part of the ATP binding pocket"
FT Binding-site 80 /note= "This residue is part of the ATP binding pocket"
FT Binding-site 91..93 /note= "These residues are part of the ATP binding pocket"
FT Binding-site 104 /note= "This residue is part of the ATP binding pocket"
FT Binding-site 108 /note= "This residue is part of the ATP binding pocket"
FT Binding-site 118 /note= "This residue is part of the ATP binding pocket"
FT Binding-site 136 /note= "This residue is part of the ATP binding pocket"
FT Binding-site 138..141 /note= "These residues are part of the ATP binding pocket"
FT Binding-site 144..145 /note= "These residues are part of the ATP binding pocket"
FT Binding-site 147 /note= "This residue is part of the substrate binding pocket"
FT Active-site 151 /note= "This residue is part of the substrate binding pocket"
FT Active-site 158 /note= "This residue is part of the substrate binding pocket"
FT Active-site 160..161 /note= "These residues are part of the substrate binding pocket"
FT Active-site 164 /note= "This residue is part of the substrate binding pocket"
FT Active-site 185..186 /note= "These residues are part of the substrate binding pocket"
FT Active-site 188..190 /note= "These residues are part of the substrate binding pocket"
FT Binding-site 190..191 /note= "These residues are part of the ATP binding pocket"
FT Binding-site 193 /note= "This residue is part of the ATP binding pocket"
FT Binding-site 206..207 /note= "These residues are part of the ATP binding pocket"
FT Active-site 210 /note= "This residue is part of the substrate binding pocket"
FT Region 217..235 /note= "Activation loop"
FT Active-site 240 /note= "This residue is part of the substrate binding pocket"
FT Active-site 244 /note= "This residue is part of the substrate binding pocket"
FT Active-site 247..248 /note= "These residues are part of the substrate binding pocket"
FT Active-site 251..252 /note= "These residues are part of the substrate binding pocket"
FT Active-site 256..257 /note= "These residues are part of the substrate binding pocket"
FT Active-site 259..261

FT Domain /note= "These residues are part of the substrate binding pocket"
FT Modified-site 328..400 /note= C-terminal regulatory domain
FT Modified-site 334 /note= "Thr is optionally O-phosphorylated. This is a major regulatory phosphorylation site"
FT Modified-site 338 /note= "Thr is optionally O-phosphorylated. This is an auto-phosphorylation site"
FT Region 345..368 /note= "Nuclear export signal (NES) motif"
FT Region 373..389 /note= "Nuclear localisation signal motif"
FT Binding-site 385..389 /note= "Docking site for activator protein p38"
PN WO2003048340-A2.
XX 12-JUN-2003.
XX PD
XX XX
XX PF
XX 05-DEC-2002; 2002WO-US039070.
XX 05-DEC-2001; 2001US-0337513P.
XX (VERT-) VERTEX PHARM INC.
PI Meng W, Swenson L;
XX WPI; 2003-482712/45.
DR
XX Crystalline molecule comprising an ATP binding pocket, substrate binding pocket or nuclear export signal binding pocket of mitogen activated protein activated protein kinase-2, useful for designing binding compounds.
PS Claim 1; SEQ ID NO 1; 172pp; English.
XX
CC The invention relates to the crystal structure of mitogen activated protein kinase activated protein kinase 2 (MAPKAPK2), its homologues and molecular complexes comprising MAPKAPK2. The MAPKAPK2 crystal structure comprises the ATP binding pocket, the substrate binding pocket and the nuclear export signal (NES) motif. MAPKAPK2 is an intracellular component of the MAP kinase signal transduction pathway that is triggered in response to cellular stresses such as heat or osmotic shock, bacterial lipopolysaccharide, proinflammatory cytokines and TNF-alpha (tumour necrosis factor-alpha). It is located in the nucleus of unstimulated cells and rapidly moves to the cytoplasm on activation by the kinases p38/p40/RK. While in the nucleus, MAPKAPK2 contributes to the phosphorylation of CREB (cAMP response element-binding protein), and is also responsible for phosphorylating serum response factor and the transcription factor E47. In the cytoplasm, MAPKAPK2 phosphorylates the small heat shock protein HSP25/HSP27, lymphocyte specific protein (LSP1), glycogen synthase, tyrosine hydroxylase (the rate-limiting enzyme in catecholamine synthesis) and 5-lipoxygenase, a key enzyme in leukotriene biosynthesis. Mice which lack MAPKAPK2 show increased stree resistance and survive bacterial LPS-induced endotoxic shock due to a 90% reduction in the production of TNF-alpha. The crystal structure of MAPKAPK2 may be used to evaluate the ability of a chemical entity to interact with binding pockets or other key domains of MAPKAPK2, and in rational drug design. MAPKAPK2-specific agonists and antagonists identified using the crystal structure may be used in the treatment of disorders related to MAPKAPK2. The present sequence represents MAPKAPK2.
SQ Sequence 400 AA;
Query Match 100.0%; Score 2106; DB 7; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.1e-161;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQGQSPVPFPAPAPPPQPPTPALPHPPAQQPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 60
Db 5 SQGQSPVPFPAPAPPPQPPTPALPHPPAQQPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 64

Db 230 DMWSLGVIMYILLCGYPFFYSNHGLAISPGMKTRIRMGQYEFNPPEWSEVSEVKMLIRN 289
QY 301 LLKTEPTQRMWITTEFMNHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 360
Db 290 LLKTEPTQRMWITTEFMNHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 349
QY 361 VDYEQIKIKKIEDASNPLLLKRRKKARALEAAALAH 396
Db 350 VDYEQIKIKKIEDASNPLLLKRRKKARAVEDAALAH 385
RESULT 10
ID ADD47657 standard; protein; 385 AA.
XX
AC ADD47657;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein CAA54183, SEQ ID NO 13353.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
OS Unidentified.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; CAA54183.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Example 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 385 AA;
Query Match 91.2%; Score 1921; DB 7; Length 385;
Best Local Similarity 92.7%; Pred. No. 1.7e-146;
Matches 367; Conservative 7; Mismatches 8; Indels 14; Gaps 2;
QY 1 SQQSPPVFPAPAPPPQPPPALPHPPAPPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 60
Db 4 SPGQTPPAPFPSPPPP-----APAQPPP----FPQFHVKSGLQIRKNAITDDYK 49
QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVY 120
Db 50 VTSQVLGLGINGKVLRIFDKRTQOKFALKMLQDCPKARREVELTWRASQCPHIVHIVDVY 109
QY 121 ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDQAFTEREASEIMKSIGEAIQYLHSINIAH 180
Db 110 ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDQAFTEREASEIMKSIGEAIQYLHSINIAH 169
QY 181 RDVKPENLLYTSKRPNAILKLTDFGPAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 240
Db 170 RDVKPENLLYTSKRPNAILKLTDFGPAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 229
QY 241 DMWSLGVIMYILLCGYPFFYSNHGLAISPGMKTRIRMGQYEFNPPEWSEVSEVKMLIRN 300
Db 230 DMWSLGVIMYILLCGYPFFYSNHGLAISPGMKTRIRMGQYEFNPPEWSEVSEVKMLIRN 289
QY 301 LLKTEPTQRMWITTEFMNHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 360
Db 290 LLKTEPTQRMWITTEFMNHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVKEEMTSALATMR 349
QY 361 VDYEQIKIKKIEDASNPLLLKRRKKARALEAAALAH 396
Db 350 VDYEQIKIKKIEDASNPLLLKRRKKARAVEDAALAH 385
RESULT 11
ABM82670
ID ABM82670 standard; protein; 378 AA.
XX
AC ABM82670;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:2919.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN41322.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 378 AA;

Query Match 89.6%; Score 1886; DB 8; Length 378;
Best Local Similarity 99.2%; Pred. No. 1.1e-143;
Matches 350; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SQGQSPVPFPAPAPPQPTPALPHPPAQQPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 60
Db |||||
5 SQGQSPVPFPAPAPPQPTPALPHPPAQQPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 64
||
QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIDVY 120
Db |||||
65 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIDVY 124
||
QY 121 ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIOYLSINIAH 180
Db |||||
125 ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIOYLSINIAH 184
||
QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 240
Db |||||
185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 244
||
QY 241 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPNPEWSEVSEVKMLIRN 300
Db |||||
245 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPNPEWSEVSEVKMLIRN 304
||
QY 301 LLKTEPTQRMTEIFMNHWPIMQSTKVPQTPPLHTSRVLKEDKERWEDVKEEMT 353
Db |||||
305 LLKTEPTQRMTEIFMNHWPIMQSTKVPQTPPLHTSRVLKEDKERWEDVKRGVT 357
||

RESULT 12
ABP54949
ID ABP54949 standard; protein; 370 AA.
XX
AC ABP54949;
XX
DT 13-JAN-2003 (first entry)
XX
DE Human MAPKAP kinase 2.
XX
KW MAPKAP kinase 2; tyrosine threonine kinase; TTK; protein kinase; enzyme;
KW mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;

KW human; gene therapy.
XX Homo sapiens.
XX WO200268444-A1.
XX
PD 06-SEP-2002.
XX
PF 21-FEB-2002; 2002WO-US005278.
XX
PR 21-FEB-2001; 2001US-0271254P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Reinhard C, Jefferson AB, Chan VW;
XX
DR WPI; 2002-698650/75.
DR N-PSDB; ABV73995.
XX
PT Reducing growth of cancer cells comprises reducing Tyrosine Threonine
PT Kinase (TTK) activity, useful in diagnosing and treating disorders with
PT abnormal expression levels and activity of TTK, such as lung, colon,
PT prostate and ovarian cancer.
XX
PS Disclosure; Page 108; 113pp; English.
XX
CC The present sequence is the protein sequence of human MAPKAP kinase 2.
CC This is an example of a gene product that is differentially expressed in
CC cancer cells relative to non-cancer cells, or between cancer cells of
CC different malignant potential. Such genes, and their gene products, can
CC be assayed in addition to tyrosine threonine kinase (TTK, see ABP54938),
CC in methods of the invention for differential expression in a test cell.
CC The invention is based on the finding that TTK is differentially
CC expressed in various forms of cancer. Methods are provided for the
CC identification of cancerous cells, especially breast cancer and colon
CC cancer cells, by detection of expression levels of TTK, as well as
CC diagnostic, prognostic and therapeutic methods based on differential
CC expression. These methods can be used as the basis of rational therapy.
CC Assays for identifying molecules that modulate the activity of these
CC genes in cancers, as well as methods of inhibiting tumour growth by
CC inhibiting the activity of TTK are also provided
XX
SQ Sequence 370 AA;

Query Match 89.4%; Score 1882; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 2.3e-143;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGQSPVPFPAPAPPQPTPALPHPPAQQPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 60
Db |||||
5 SQGQSPVPFPAPAPPQPTPALPHPPAQQPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 64
||
QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIDVY 120
Db |||||
65 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIDVY 124
||
QY 121 ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIOYLSINIAH 180
Db |||||
125 ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIOYLSINIAH 184
||
QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 240
Db |||||
185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 244
||
QY 241 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPNPEWSEVSEVKMLIRN 300
Db |||||
245 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFNPNPEWSEVSEVKMLIRN 304
||
QY 301 LLKTEPTQRMTEIFMNHWPIMQSTKVPQTPPLHTSRVLKEDKERWEDVK 349
Db |||||
305 LLKTEPTQRMTEIFMNHWPIMQSTKVPQTPPLHTSRVLKEDKERWEDVK 353
||

RESULT 13
ABU61622
ID ABU61622 standard; protein; 370 AA.
XX
AC ABU61622;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human cancer-expressed protein MAPKAP kinase 2.
XX
KW Human; enzyme; tyrosine threonine kinase; TTK; cancer; cytostatic;
KW mitotic checkpoint gene; MAPKAP kinase 2.
XX
OS Homo sapiens.
XX
PN US2003045491-A1.
XX
PD 06-MAR-2003.
XX
PF 21-FEB-2002; 2002US-00081119.
XX
PR 23-FEB-2001; 2001US-0289813P.
XX
PA (REIN/) REINHARD C.
PA (JEFF/) JEFFERSON A B.
PA (CHAN/) CHAN V W.
XX
PI Reinhard C, Jefferson AB, Chan VW;
XX
DR WPI; 2003-456566/43.
DR N-PSDB; ACA62272.
XX
PT Detecting cancer in a subject, by comparing expression levels of tyrosine
PT threonine kinase polypeptide or polynucleotide in a subject cell and a
PT normal cell, where an increase in the expression level in the test cell
PT is indicative of cancer.
XX
PS Disclosure; Page 61-62; 79pp; English.
XX
CC The invention relates to detecting cancer (other than ovarian cancer) in
CC a subject, comprising comparing the expression levels of tyrosine
CC threonine kinase (TTK, a mitotic checkpoint gene) polypeptide or
CC polynucleotide in a test cell obtained from the subject and in a normal
CC non-cancer cell, where an increase in the expression level of TTK protein
CC or nucleic acid in the test cell compared to that in the normal cell,
CC indicates the presence of cancer other than ovarian cancer. Also included
CC are reducing growth of a cancerous cell (by contacting a cancerous cell
CC with an amount of an agent effective to reduce TTK polypeptide activity
CC in the cell), an assay for identifying a candidate agent that reduces
CC growth of a cancerous cell (comprising: (i) detecting the activity of a
CC TTK polypeptide in the presence of a candidate agent; and (ii) comparing
CC the activity of TTK polypeptide in the presence of a candidate agent
CC relative to TTK polypeptide activity in the absence of the candidate
CC agent), identifying an agent that reduces TTK activity (comprising: (i)
CC contacting a cancerous cell displaying elevated expression of a TTK-
CC encoding polynucleotide with a candidate agent; and (ii) determining the
CC effect of the candidate agent on TTK polypeptide activity) and assessing
CC the prognosis of a cancerous disease other than ovarian cancer in a
CC subject (comprising: (i) detecting expression of TTK -encoding
CC polynucleotide in a test cancer cell of a subject; and (ii) comparing a
CC level of expression of TTK-encoding polynucleotide in the test cancer
CC cell with a level of expression of the polynucleotide in a control non-
CC cancer cell, where the level of expression of TTK in the test cancer cell
CC relative to the level of expression in the control non-cancer cell is
CC indicative of the prognosis of the cancerous disease). The methods are
CC useful for detecting cancer (other than ovarian cancer) in a subject,
CC reducing growth of cancerous cells, identifying a candidate agent that
CC reduces growth of a cancerous cell, identifying an agent that reduces TTK
CC activity and assessing the prognosis of a cancerous disease other than
CC ovarian cancer. The methods are also useful for determining the ability
CC of a subject to respond to a particular therapy e.g. as a basis of
CC rational therapy. The present sequence represents another protein which
CC is differentially expressed in cancer tissues, in this case human MAPKAP

CC kinase 2
XX
SQ Sequence 370 AA;

Query Match 89.4%; Score 1882; DB 7; Length 370;
Best Local Similarity 100.0%; Pred. No. 2.3e-143;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGSPVPVFPAPAPPPQPPFPALPHPPAQP PPPPPQFPQFHVKSLQIKGNAIIDDYK 60
Db 5 SQGSPVPVFPAPAPPPQPPFPALPHPPAQP PPPPPQFPQFHVKSLQIKGNAIIDDYK 64

QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIDVY 120
Db 65 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIDVY 124

QY 121 ENLYAGRKCLLI VMECLDGGELFSRIQDRGDQAFTEREASEIMKSIGEAIQYLHSINIAH 180
Db 125 ENLYAGRKCLLI VMECLDGGELFSRIQDRGDQAFTEREASEIMKSIGEAIQYLHSINIAH 184

QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 240
Db 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 244

QY 241 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYFFPNPEWSEVSEVKMLIRN 300
Db 245 DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYFFPNPEWSEVSEVKMLIRN 304

QY 301 LLKTEPTQRM TITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 349
Db 305 LLKTEPTQRM TITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 353

RESULT 14
ADM36338
ID ADM36338 standard; protein; 370 AA.
XX
AC ADM36338;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human MK2 variant 1 protein SEQ ID NO:2.
XX
KW ischaemic injury;
KW mitogen-activated protein kinase-activated protein kinase 2; MK2;
KW vasotropic; cerebroprotective; cardiant; hypotensive;
KW antiarteriosclerotic; thrombolytic; neuroprotective; cardiovascular;
KW antianginal; antiarrhythmic; MK2 antagonist; cerebral ischaemia;
KW ischaemia; vascular occlusion; cerebral infarction; stroke;
KW cerebral vascular disease; myocardial infarction;
KW coronary artery disease; congestive heart failure; cardiac arrhythmia;
KW unstable angina; high blood pressure; claudication;
KW peripheral occlusive arterial disease; atherosclerosis;
KW thrombotic condition; thromboembolic condition; CNS disorder; human;
KW MK2 variant 1; chromosome 1q32.
XX
OS Homo sapiens.
XX
PN WO2004017909-A2.
XX
PD 04-MAR-2004.
XX
PF 21-AUG-2003; 2003WO-US026337.
XX
PR 23-AUG-2002; 2002US-0405586P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Wang X, Schieven G, Feuerstein GZ;
XX
DR WPI; 2004-226726/21.
DR N-PSDB; ADM36337.
XX

PT Reducing or treating ischemic injury, comprises administering an
PT inhibitor of mitogen-activated protein kinase-activated protein kinase 2
XX (MK2) activity or expression.
XX
PS Disclosure; SEQ ID NO 2; 39pp; English.
XX
CC The present invention describes a method for reducing ischaemic injury in
CC a mammal, which comprises administering a compound that reduces the
CC activity of mitogen-activated protein kinase-activated protein kinase 2
CC (MK2) or that inhibits MK2 expression. Also described: (1) identifying a
CC compound which inhibits MK2 expression in a cell, or which modulates MK2
CC activity; (2) compounds identified by the method above; and (3) treating
CC ischaemic injury by administering to a patient a compound above, or an
CC MK2 modulator. The compound has vasotropic, cerebroprotective, cardiant,
CC hypotensive, antiarteriosclerotic, thrombolytic, neuroprotective,
CC cardiovascular, antianginal and antiarrhythmic activities, and can be
CC used as an MK2 antagonist. The method is useful reducing or treating
CC ischaemic injury, particularly cerebral ischaemia. Compounds identified
CC by the method are useful for treating ischaemia, (e.g. ischaemia
CC resulting from vascular occlusion, cerebral infarction, stroke, and
CC related cerebral vascular diseases), myocardial infarction, coronary
CC artery disease, congestive heart failure, cardiac arrhythmias, unstable
CC angina, high blood pressure, claudication, peripheral occlusive arterial
CC disease, atherosclerosis, thrombotic or thromboembolic conditions, or CNS
CC disorders associated with cerebral ischaemia. The present sequence
CC represents the human MK2 variant 1, which is located on chromosome 1q32.
XX
SQ Sequence 370 AA;

Query Match 89.4%; Score 1882; DB 8; Length 370;
Best Local Similarity 100.0%; Pred. No. 2.3e-143;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQGQSPVPFPAPAPPPQPTPALPHPPAQPPPPPPQFPQFHVKSGLIQKNAIIDDYK 60
DB 5 SQGQSPVPFPAPAPPPQPTPALPHPPAQPPPPPPQFPQFHVKSGLIQKNAIIDDYK 64
QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120
DB 65 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 124
QY 121 ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 180
DB 125 ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 184
QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTTPCYTPYYVAPEVLGPEKYDKSC 240
DB 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTTPCYTPYYVAPEVLGPEKYDKSC 244
QY 241 DMWSLGVIMYILLCGYPPFFSYNHGLAISPGMKTRIRMGQYEFPPNPEWSEVSEVKMLIRN 300
DB 245 DMWSLGVIMYILLCGYPPFFSYNHGLAISPGMKTRIRMGQYEFPPNPEWSEVSEVKMLIRN 304
QY 301 LLKTEPTQRTMTITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 349
DB 305 LLKTEPTQRTMTITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 353

RESULT 15
ADP87579
ID ADP87579 standard; protein; 370 AA.
XX
AC ADP87579;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human NOVX polypeptide, NOV3a.
XX
KW anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes;
KW insulin resistance; hybridization probe; chromosome mapping;
KW tissue typing; preventive medicine; pharmacogenomics; NOVX; human.
XX
OS Homo sapiens.

XX WO2004056961-A2.
PN
XX
PD 08-JUL-2004.
XX
PF 27-OCT-2003; 2003WO-US034114.
XX
PR 25-OCT-2002; 2002US-0421239P.
PR 28-OCT-2002; 2002US-0421700P.
PR 31-OCT-2002; 2002US-0422776P.
PR 13-NOV-2002; 2002US-0426197P.
PR 20-DEC-2002; 2002US-0435498P.
PR 20-DEC-2002; 2002US-0435510P.
PR 20-DEC-2002; 2002US-0435568P.
PR 21-MAR-2003; 2003US-0456812P.
XX (CURA-) CURAGEN CORP.
PA
XX
XX Berghs C, Catterton E, Ellerman K, Ort T, Rieger D, Chaudhuri A;
PI
XX
XX WPI; 2004-500293/47.
DR N-PSDB; ADP87578.
XX
PT New NOVX nucleic acid molecules and polypeptides useful for preventing or
PT treating NOVX-associated disorders, e.g. diabetes, insulin resistance or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Claim 3; SEQ ID NO 34; 570pp; English.
XX
CC The invention relates to a novel isolated nucleic acid molecule
CC comprising any of the nucleotide sequences (e.g. 3634, 2127 or 2120 base
CC pairs) fully defined in the specification; or encodes any of the amino
CC acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the
CC specification. The invention further comprises: an isolated polypeptide
CC comprising any of the amino acid sequences cited above; a method for
CC identifying compounds that modulate target polypeptide activity; an
CC antibody that immunospecifically binds to the target polypeptide; where
CC the target polypeptide comprises any of the above-mentioned amino acid
CC sequences, an amino acid sequence that is at least 95% identical to the
CC above amino acid sequences, an amino acid sequence of at least one domain
CC of the above-mentioned amino acid sequences, or an amino acid sequence
CC that is at least 95% identical to the domain of the above amino acid
CC sequences; a method for identifying a potential therapeutic agent for use
CC in treatment of a pathology, where the pathology is related to aberrant
CC expression or aberrant physiological interactions of a target polypeptide
CC; and a method of screening for a modulator of activity of or of latency
CC or predisposition to a pathology associated with a target polypeptide.
CC The modulating compounds have anorectic and antidiabetic activities. The
CC nucleic acid sequences of the invention may be used in gene therapy to
CC treat disorders. The proteins of the invention may be used in creating a
CC vaccine. The composition and methods are useful for identifying compounds
CC that modulate protein activity or for diagnosing, preventing or treating
CC diverse pathological conditions, such as obesity, diabetes or insulin
CC resistance. The nucleic acids are also used as hybridization probes, in
CC chromosome mapping, tissue typing, preventive medicine, and
CC pharmacogenomics. This sequence represents a NOVX polypeptide of the
CC invention.
XX
SQ Sequence 370 AA;

Query Match 89.4%; Score 1882; DB 8; Length 370;
Best Local Similarity 100.0%; Pred. No. 2.3e-143;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SQGQSPVPFPAPAPPPQPTPALPHPPAQPPPPPPQFPQFHVKSGLIQKNAIIDDYK 60
DB 5 SQGQSPVPFPAPAPPPQPTPALPHPPAQPPPPPPQFPQFHVKSGLIQKNAIIDDYK 64
QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120
DB 65 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 124
QY 121 ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 180

Db	125	ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH	184
Qy	181	RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC	240
Db	185	RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC	244
Qy	241	DMWSLGVIMYILLCGYPPFPFYSNHGLAISPGMKTRIRMGQYEFPPNPWSEVSEEVKMLIRN	300
Db	245	DMWSLGVIMYILLCGYPPFPFYSNHGLAISPGMKTRIRMGQYEFPPNPWSEVSEEVKMLIRN	304
Qy	301	LLKTEPTQRMTTTEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK	349
Db	305	LLKTEPTQRMTTTEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK	353

Search completed: June 19, 2006, 08:54:45
Job time : 202 secs

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Run on: June 19, 2006, 09:12:12 ; Search time 188 Seconds
(without alignments)
975.708 Million cell updates/sec
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2106	100.0	396	4	US-10-469-221-2
2	2106	100.0	400	4	US-10-116-649-1
3	2106	100.0	400	4	US-10-294-027-1
4	2106	100.0	400	4	US-10-469-221-4
5	2106	100.0	400	5	US-10-497-767-1
6	2097	99.6	400	4	US-10-645-190-4
7	1882	89.4	370	4	US-10-081-119-34
8	1882	89.4	370	4	US-10-645-190-2
9	1882	89.4	370	5	US-10-951-389-34
10	1882	89.4	370	5	US-10-951-406-34
11	1882	89.4	370	5	US-10-951-477-34
12	1882	89.4	370	5	US-10-977-087-34
13	1833	87.0	357	4	US-10-664-421-114
14	1833	87.0	357	5	US-10-941-635-115
15	1729	82.1	327	4	US-10-116-649-2
16	1729	82.1	434	4	US-10-338-411-29
17	1729	82.1	434	4	US-10-389-640-29
18	1716	81.5	326	4	US-10-294-027-4
19	1391	66.0	382	4	US-10-294-027-2
20	1391	66.0	382	5	US-10-497-767-2
21	1391	66.0	382	5	US-10-501-035-352
22	1201	57.0	359	6	US-11-097-143-5664
23	1201	57.0	359	6	US-11-097-143-29037
24	1046	49.7	443	4	US-10-369-493-5950
25	995	47.2	197	3	US-09-925-300-1178
26	796.5	37.8	521	4	US-10-369-493-5500
27	733	34.8	471	5	US-10-770-726-68
					Sequence 2, Appli
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 4, Appli
					Sequence 1, Appli
					Sequence 4, Appli
					Sequence 34, Appli
					Sequence 2, Appli
					Sequence 34, Appli
					Sequence 34, Appli
					Sequence 34, Appli
					Sequence 34, Appli
					Sequence 114, App
					Sequence 115, App
					Sequence 2, Appli
					Sequence 29, Appli
					Sequence 29, Appli
					Sequence 4, Appli
					Sequence 2, Appli
					Sequence 352, App
					Sequence 5664, Ap
					Sequence 29037, A
					Sequence 5950, Ap
					Sequence 1178, Ap
					Sequence 5500, Ap
					Sequence 68, Appli

ALIGNMENTS

RESULT 1

US-10-469-221-2
; Sequence 2, Application US/10469221
; Publication No. US20040170995A1
; GENERAL INFORMATION:
; APPLICANT: LOGRASSO, PHILIP
; APPLICANT: HAWKINS, JULIO
; APPLICANT: LISNOCK, JEAN MARIE
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: A NOVEL HUMAN SIGNAL TRANSDUCING KINASE-MAPKAP-2; ENCODED
; TITLE OF INVENTION: PROTEINS, CELLS TRANSFORMED THEREWITH AND USES THEREOF
; FILE REFERENCE: 20813P
; CURRENT APPLICATION NUMBER: US/10/469,221
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: PCT/US02/05670
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/272,260
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Human
US-10-469-221-2

Query Match 100.0%; Score 2106; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 4.5e-133;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	SQGSPPVPFPAPAPPPQPTPALPHPPAQPPPPPPQFPQFHVKSLQIKKNAIIDDYK	60
Db	1	SQGSPPVPFPAPAPPPQPTPALPHPPAQPPPPPPQFPQFHVKSLQIKKNAIIDDYK	60
QY	61	VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVY	120
Db	61	VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVY	120
QY	121	ENLYAGRKCLLIVMECLDGGELFSRIQDRGDAFTEREASEIMKSIGEAIOYLHSINIAH	180
Db	121	ENLYAGRKCLLIVMECLDGGELFSRIQDRGDAFTEREASEIMKSIGEAIOYLHSINIAH	180
QY	181	RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNSLTPCYTPYYVAPEVLGPEKYDKSC	240
Db	181	RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNSLTPCYTPYYVAPEVLGPEKYDKSC	240
QY	241	DMWSLGVIMYILLCGYPPFFYSNHGLAISPGMKTRIRMGQYEFPPNPEWSEVSEEVKMLIRN	300
Db	241	DMWSLGVIMYILLCGYPPFFYSNHGLAISPGMKTRIRMGQYEFPPNPEWSEVSEEVKMLIRN	300

		; NUMBER OF SEQ ID NOS: 4		Query Match		100.0%; Score 2106; DB 4; Length 400;	
		; SOFTWARE: FastSEQ for Windows Version 4.0		Best Local Similarity		100.0%; Pred. No. 4.5e-133;	
		; SEQ ID NO 4		Matches 396; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
		; LENGTH: 400					
		; TYPE: PRT					
		; ORGANISM: Human					
		US-10-469-221-4					
QY	1	SQGSPPVPFPAPAPPPQPTPALPHPPAQP	PPPPPPQFPQFHVKSGLQIKKNAI	DDYK	60		
Db	5	SQGSPPVPFPAPAPPPQPTPALPHPPAQP	PPPPPPQFPQFHVKSGLQIKKNAI	DDYK	64		
QY	61	VTSQVLGLGINGKVLQIFNKR	TQEFALKMLQDCPKARREVELHWRASQC	PHIVRIVDVY	120		
Db	65	VTSQVLGLGINGKVLQIFNKR	TQEFALKMLQDCPKARREVELHWRASQC	PHIVRIVDVY	124		
QY	121	ENLYAGRKCLLI	VMECLDGGELFSRIQDRGDAFTEREASEIMKSIG	EAIQYLHSINIAH	180		
Db	125	ENLYAGRKCLLI	VMECLDGGELFSRIQDRGDAFTEREASEIMKSIG	EAIQYLHSINIAH	184		
QY	181	RDVKPENLLYTSKRPNAILKLTDFG	FAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC	240			
Db	185	RDVKPENLLYTSKRPNAILKLTDFG	FAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC	244			
QY	241	DMWSLGVIMYILLCGYP	PPFYSNHGLAISP	GMKTIRMGQYEFNP	PEWSEVSEVKMLIRN	300	
Db	245	DMWSLGVIMYILLCGYP	PPFYSNHGLAISP	GMKTIRMGQYEFNP	PEWSEVSEVKMLIRN	304	
QY	301	LLKTEPTQRM	TI	TEFMNHPWIMQSTKVPQ	TPLHTSRVLKEDKERWEDVKEEMTSALATMR	360	
Db	305	LLKTEPTQRM	TI	TEFMNHPWIMQSTKVPQ	TPLHTSRVLKEDKERWEDVKEEMTSALATMR	364	
QY	361	VDYEQIKIKKIEDASNP	LLLRKKKARALEAA	LAH	396		
Db	365	VDYEQIKIKKIEDASNP	LLLRKKKARALEAA	LAH	400		
RESULT 5							
US-10-497-767-1							
; Sequence 1, Application US/10497767							
; Publication No. US20050261836A1							
; GENERAL INFORMATION:							
; APPLICANT: VERTEX PHARMACEUTICALS INCORPORATED							
; APPLICANT: MENG, WUYI							
; APPLICANT: SWENSON, LOVORKA							
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF MITOGEN-ACTIVATED PROTEIN							
; TITLE OF INVENTION: KINASE-ACTIVATED PROTEIN KINASE 2 AND BINDING POCKETS							
; TITLE OF INVENTION: THEREOF							
; FILE REFERENCE: VP1/01-13 PCT							
; CURRENT APPLICATION NUMBER: US/10/497,767							
; CURRENT FILING DATE: 2004-06-04							
; PRIOR APPLICATION NUMBER: 60/337,513							
; PRIOR FILING DATE: 2001-12-05							
; NUMBER OF SEQ ID NOS: 15							
; SOFTWARE: PatentIn Ver. 2.1							
; SEQ ID NO 1							
; LENGTH: 400							
; TYPE: PRT							
; ORGANISM: Homo sapiens							
US-10-497-767-1							
Query Match		100.0%; Score 2106; DB 5; Length 400;					
Best Local Similarity		100.0%; Pred. No. 4.5e-133;					
Matches 396; Conservative		0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	SQGSPPVPFPAPAPPPQPTPALPHPPAQP	PPPPPPQFPQFHVKSGLQIKKNAI	DDYK	60		
Db	5	SQGSPPVPFPAPAPPPQPTPALPHPPAQP	PPPPPPQFPQFHVKSGLQIKKNAI	DDYK	64		

Qy	361	VDYEQIKIKKIEDASNP	LLKRRKKARALEAA	LAH	396
D _b	365	VDYEQIKIKKIEDASNP	LLKRRKKARALEAA	LAH	400

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RESULT 7
US-10-081-119-34
; Sequence 34, Application US/10081119
; Publication No. US20030045491A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/081,119
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-081-119-34

```

```
Query Match      89.4%; Score 1882; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 4.4e-118;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1	SQGSPPVPFPAPAPPPQPPPTPALPHEPPAQPPPPPPQPPQFPHVKSGLQIKKNAIIDDK	60
Db	5	SQGSPPVPFPAPAPPPQPPPTPALPHEPPAQPPPPPPQPPQFPHVKSGLQIKKNAIIDDK	64
QY	61	VTSQVLGLGINGKVLQIFNKRTQEFALKMLQDCPKARREVELHWRASQCPHIVRVDVY	120
Db	65	VTSQVLGLGINGKVLQIFNKRTQEFALKMLQDCPKARREVELHWRASQCPHIVRVDVY	124
QY	121	ENLYAGRKCLLI VMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH	180
Db	125	ENLYAGRKCLLI VMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH	184
QY	181	RDVKPENLLYTSKRPNAILKLTDFGAKETTSHNSLTTTCYTPYYVAPEVLGPEKYDKSC	240
Db	185	RDVKPENLLYTSKRPNAILKLTDFGAKETTSHNSLTTTCYTPYYVAPEVLGPEKYDKSC	244
QY	241	DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFPPNPWSEVSEVKMLIRN	300
Db	245	DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEFPPNPWSEVSEVKMLIRN	304
QY	301	LLKTEPTQRMTTITEFMNHPWIMQSTKVPQTPPLHTSRVLKEDKERWEDVK	349
Db	305	LLKTEPTQRMTTITEFMNHPWIMOSTKVPQTPPLHTSRVLKEDKERWEDVK	353

RESULT 8
US-10-645-190-2
; Sequence 2, Application US/10645190
; Publication No. US20040110710A1
; GENERAL INFORMATION:
; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
; TITLE OF INVENTION: METHODS FOR PREVENTING ISCHEMIC BRAIN INJURY
; FILE REFERENCE: D0299 NP
; CURRENT APPLICATION NUMBER: US/10/645,190
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/405,586
; PRIOR FILING DATE: 2002-08-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: RatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 370

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; TYPE: PRT
; ORGANISM: Human
US-10-645-190-2

      89.4%; Score 1882; DB 4; Length 370;
Best Local Similarity 100.0%; Pred. No. 4.4e-118;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  SQQSPPVPFPAPAPPQPTPALPHPPAQQPPPPPPQFPQFHVKSGLOIKKNAIIDDYK 60
      |||
Db      5  SQQSPPVPFPAPAPPQPTPALPHPPAQQPPPPPPQFPQFHVKSGLOIKKNAIIDDYK 64

QY     61  VTSQVLGLGINGKVLQIFNKRTQEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120
      |||
Db     65  VTSQVLGLGINGKVLQIFNKRTQEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 124

QY    121  ENLYAGRKCLLI VMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 180
      |||
Db    125  ENLYAGRKCLLI VMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 184

QY    181  RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 240
      |||
Db    185  RDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYYVAPEVLGPEKYDKSC 244

QY    241  DMWSLGVIMYILLCGYPPFYSNHGLAISPGMKTRIRMGQYEFPPNPESVSEEVKMLIRN 300
      |||
Db    245  DMWSLGVIMYILLCGYPPFYSNHGLAISPGMKTRIRMGQYEFPPNPESVSEEVKMLIRN 304

QY    301  LLKTEPTQRMITITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 349
      |||
Db    305  LLKTEPTQRMITITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 353

```

```

RESULT 9
US-10-951-389-34
; Sequence 34, Application US/10951389
; Publication No. US20050058627A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,389
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-389-34

```

	Query Match	89.4%;	Score 1882;	DB 5;	Length 370;
	Best Local Similarity	100.0%;	Pred. No. 4.4e-118;		
	Matches 349;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	SQSQSPVPFPAPAPPQPTPALPHPPAQPPPPPPQFPQFHVKSGLQIKKNAIIDYK	60		
Db	5	SQSQSPVPFPAPAPPQPTPALPHPPAQPPPPPPQFPQFHVKSGLQIKKNAIIDYK	64		
Qy	61	VTSQLGLGINGKVLQIFNKRTQEKFAKMLQDCPKARREVELHWRASQCPHIVRIDVY	120		
Db	65	VTSQLGLGINGKVLQIFNKRTQEKFAKMLQDCPKARREVELHWRASQCPHIVRIDVY	124		
Qy	121	ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH	180		
Db	125	ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH	184		

```
QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 240
|
Db 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 244
|
QY 241 DMWSLGVIMYILLCGYPPFFYSNHGLAISPGMKTRIRMGQYEFNPPEWSEVSEEVKMLIRN 300
|
Db 245 DMWSLGVIMYILLCGYPPFFYSNHGLAISPGMKTRIRMGQYEFNPPEWSEVSEEVKMLIRN 304
|
QY 301 LLKTEPTQRM TITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 349
|
Db 305 LLKTEPTQRM TITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 353
|
RESULT 10
US-10-951-406-34
; Sequence 34, Application US/10951406
; Publication No. US20050059630A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,406
; PRIOR FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-406-34
Query Match 89.4%; Score 1882; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 4.4e-118;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGQSPVPFPAPAPPQPTPALPHPPAQPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 60
|
Db 5 SQGQSPVPFPAPAPPQPTPALPHPPAQPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 64
|
QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120
|
Db 65 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 124
|
QY 121 ENLYAGRKCLLI VMECLDGGELFSRIQDRGDOAFTEREASEIMKSIGEAIOYLHSINIAH 180
|
Db 125 ENLYAGRKCLLI VMECLDGGELFSRIQDRGDOAFTEREASEIMKSIGEAIOYLHSINIAH 184
|
QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 240
|
Db 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 244
|
QY 241 DMWSLGVIMYILLCGYPPFFYSNHGLAISPGMKTRIRMGQYEFNPPEWSEVSEEVKMLIRN 300
|
Db 245 DMWSLGVIMYILLCGYPPFFYSNHGLAISPGMKTRIRMGQYEFNPPEWSEVSEEVKMLIRN 304
|
QY 301 LLKTEPTQRM TITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 349
|
Db 305 LLKTEPTQRM TITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 353
|
RESULT 11
US-10-951-477-34
; Sequence 34, Application US/10951477
; Publication No. US20050063974A1
; GENERAL INFORMATION:
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; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/951,477
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: US/10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-477-34
Query Match 89.4%; Score 1882; DB 5; Length 370;
Best Local Similarity 100.0%; Pred. No. 4.4e-118;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGQSPVPFPAPAPPQPTPALPHPPAQPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 60
|
Db 5 SQGQSPVPFPAPAPPQPTPALPHPPAQPPPPPPQFPQFHVKSGLQIKKNAIIDDYK 64
|
QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120
|
Db 65 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 124
|
QY 121 ENLYAGRKCLLI VMECLDGGELFSRIQDRGDOAFTEREASEIMKSIGEAIOYLHSINIAH 180
|
Db 125 ENLYAGRKCLLI VMECLDGGELFSRIQDRGDOAFTEREASEIMKSIGEAIOYLHSINIAH 184
|
QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 240
|
Db 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 244
|
QY 241 DMWSLGVIMYILLCGYPPFFYSNHGLAISPGMKTRIRMGQYEFNPPEWSEVSEEVKMLIRN 300
|
Db 245 DMWSLGVIMYILLCGYPPFFYSNHGLAISPGMKTRIRMGQYEFNPPEWSEVSEEVKMLIRN 304
|
QY 301 LLKTEPTQRM TITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 349
|
Db 305 LLKTEPTQRM TITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 353
|
RESULT 12
US-10-977-087-34
; Sequence 34, Application US/10977087
; Publication No. US20050130926A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; APPLICANT: Kaufmann, Joerg
; APPLICANT: Xin, Hong
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Khoja, Hamiduddin
; APPLICANT: Shyamala, Venkatakrishna
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS CELLS
; TITLE OF INVENTION: AND THEIR METHODS OF USE V
; FILE REFERENCE: 2300-21986
; CURRENT APPLICATION NUMBER: US/10/977,087
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: 10/081,119
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/271,254
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 10/360,848
; PRIOR FILING DATE: 2003-02-06
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; PRIOR APPLICATION NUMBER: 09/570,593
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134,112
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 10/763,692
; PRIOR FILING DATE: 2004-01-22
; PRIOR APPLICATION NUMBER: 09/626,301
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/148,936
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/145,612
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 10/698,959
; PRIOR FILING DATE: 2003-10-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-977-087-34

Query Match      89.4%;   Score 1882;   DB 5;   Length 370;
Best Local Similarity 100.0%;   Pred. No. 4.4e-118;
Matches 349;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY 1 SQQSPPVPFPAPAPPQPTPALPHPPAQPPTPPQFPQFHVKSGLIQKNAIIDDYK 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5 SQQSPPVPFPAPAPPQPTPALPHPPAQPPTPPQFPQFHVKSGLIQKNAIIDDYK 64

QY 61 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 65 VTSQVLGLGINGKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRVDVY 124

QY 121 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 180
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Db 125 ENLYAGRKCLLIWMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAH 184

QY 181 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 240
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 185 RDVKPENLLYTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSC 244

QY 241 DMWSLGVIMYILLCGYPPFYSNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRN 300
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 245 DMWSLGVIMYILLCGYPPFYSNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRN 304

QY 301 LLKTEPTQRTITEFMNHPWIMQSTKVPQTPLTHTSRVLKEDKERWEDVK 349
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 305 LLKTEPTQRTITEFMNHPWIMQSTKVPQTPLTHTSRVLKEDKERWEDVK 353

RESULT 13
US-10-664-421-114
; Sequence 114, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 114
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; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-664-421-114

Query Match      87.0%;   Score 1833;   DB 4;   Length 357;
Best Local Similarity 100.0%;   Pred. No. 8.1e-115;
Matches 340;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY 10 FPAPAPPPQPTPALPHPPAQPPTPPQFPQFHVKSGLIQKNAIIDDYKVTSQLGLG 69
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QY 70 INKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVYENLYAGRKC 129
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Db 61 INKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVYENLYAGRKC 120

QY 130 LLIVMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAHRDVKPENLL 189
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 LLIVMECLDGGELFSRIQDRGDAQFTEREASEIMKSIGEAIQYLHSINIAHRDVKPENLL 180

QY 190 YTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSCDMWSLGVIM 249
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 YTSKRPNAILKLTDFGFAKETTSNLSLTPCYTPYYVAPEVLGPEKYDKSCDMWSLGVIM 240

QY 250 YILLCGYPPFYSNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRNLLKTEPTQR 309
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 YILLCGYPPFYSNHGLAISPGMKTRIRMGQYEFNPEWSEVSEVKMLIRNLLKTEPTQR 300

QY 310 MTITEFMNHPWIMQSTKVPQTPLTHTSRVLKEDKERWEDVK 349
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Db 301 MTITEFMNHPWIMQSTKVPQTPLTHTSRVLKEDKERWEDVK 340

RESULT 14
US-10-941-635-115
; Sequence 115, Application US/10941635
; Publication No. US20050164300A1
; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HURT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 115
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
;
US-10-941-635-115

Query Match      87.0%;   Score 1833;   DB 5;   Length 357;
Best Local Similarity 100.0%;   Pred. No. 8.1e-115;
Matches 340;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY 10 FPAPAPPPQPTPALPHPPAQPPTPPQFPQFHVKSGLIQKNAIIDDYKVTSQLGLG 69
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Db 1 FPAPAPPPQPTPALPHPPAQPPTPPQFPQFHVKSGLIQKNAIIDDYKVTSQLGLG 60

QY 70 INKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVYENLYAGRKC 129
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Db 61 INKVLQIFNKRTOEKFALKMLQDCPKARREVELHWRASQCPHIVRIVDVYENLYAGRKC 120
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Search completed: June 19, 2006, 09:15:34
Job time : 189 secs

QY 130 LLIVMECLDGGELFSRIQDRGDOAFTEREASEIMKSIGEAIQYLHSINIAHRDVKPENLL 189
Db 121 LLIVMECLDGGELFSRIQDRGDOAFTEREASEIMKSIGEAIQYLHSINIAHRDVKPENLL 180
QY 190 YTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYVVAPEVLGPEKYDKSCDMWSLGVM 249
Db 181 YTSKRPNAILKLTDFGFAKETTSHNSLTTPCYTPYVVAPEVLGPEKYDKSCDMWSLGVM 240
QY 250 YILLCGYPPFYSNHGLAISPGMKTRIRMGQYEFNPPEWSEVSEVKMLIRNLLKTEPTQR 309
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QY 310 MTITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 349
Db 301 MTITEFMNHPWIMQSTKVPQTPLHTSRVLKEDKERWEDVK 340

RESULT 15
US-10-116-649-2
; Sequence 2, Application US/10116649
; Publication No. US20040005686A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia
; APPLICANT: Kurumbail, Ravi G
; APPLICANT: Pawlitz, Jennifer L
; APPLICANT: Stegeman, Roderick A
; APPLICANT: Stallings, William C
; APPLICANT: Shieh, Huey S
; APPLICANT: Mourey, Robert J
; APPLICANT: Bolten, Suzanne L
; APPLICANT: Broadus, Richard M
; TITLE OF INVENTION: CRYSTALLINE STRUCTURE OF HUMAN MAPKAP Kinase-2
; FILE REFERENCE: PHA 4184.1
; CURRENT APPLICATION NUMBER: US/10/116,649
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-649-2

Query Match 82.1%; Score 1729; DB 4; Length 327;
Best Local Similarity 100.0%; Pred. No. 6.9e-108;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41 QFHVKSGLQIKKNAIIDDYKVTSQVLGLGINGKVLQIFNKRTQEKFALKMLQDCPKARRE 100
Db 1 QFHVKSGLQIKKNAIIDDYKVTSQVLGLGINGKVLQIFNKRTQEKFALKMLQDCPKARRE 60
QY 101 VELHWRASQCPHIVRIVDVYENLYAGRKCLLIWMECLDGGELFSRIQDRGDOAFTEREAS 160
Db 61 VELHWRASQCPHIVRIVDVYENLYAGRKCLLIWMECLDGGELFSRIQDRGDOAFTEREAS 120
QY 161 EIMKSIGEAIQYLHSINIAHRDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPC 220
Db 121 EIMKSIGEAIQYLHSINIAHRDVKPENLLYTSKRPNAILKLTDFGFAKETTSHNSLTTPC 180
QY 221 YTPYVVAPEVLGPEKYDKSCDMWSLGVMYIILCGYPPFYSNHGLAISPGMKTRIRMGQY 280
Db 181 YTPYVVAPEVLGPEKYDKSCDMWSLGVMYIILCGYPPFYSNHGLAISPGMKTRIRMGQY 240
QY 281 EFPNPEWSEVSEVKMLIRNLLKTEPTQRTMTITEFMNHPWIMQSTKVPQTPLHTSRVLKE 340
Db 241 EFPNPEWSEVSEVKMLIRNLLKTEPTQRTMTITEFMNHPWIMQSTKVPQTPLHTSRVLKE 300
QY 341 DKERWEDVKEEMTSALATMRVDYEQIK 367
Db 301 DKERWEDVKEEMTSALATMRVDYEQIK 327

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OM protein - protein search, using sw model

Run on: June 19, 2006, 09:12:32 ; Search time 23 Seconds
(without alignments)
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Scoring table: BLOSUM62
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Searched: 96747 seqs, 22556637 residues

Total number of hits satisfying chosen parameters: 96747

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA New:*
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5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2106	100.0	400	7	US-11-273-567-4 Sequence 4, Appli
2	1882	89.4	370	7	US-11-273-567-3 Sequence 3, Appli
3	1391	66.0	382	6	US-10-505-928-625 Sequence 625, App
4	508.5	24.1	542	6	US-10-449-902-48403 Sequence 48403, A
5	487.5	23.1	473	7	US-11-242-505A-42 Sequence 42, Appl
6	483	22.9	623	6	US-10-449-902-50362 Sequence 50362, A
7	475.5	22.6	733	6	US-10-505-928-349 Sequence 349, App
8	474.5	22.5	513	6	US-10-449-902-55199 Sequence 55199, A
9	452	21.5	574	6	US-10-449-902-36211 Sequence 36211, A
10	435.5	20.7	766	7	US-11-312-958-34 Sequence 34, Appl
11	434	20.6	568	6	US-10-449-902-46406 Sequence 46406, A
12	434	20.6	729	7	US-11-312-958-64 Sequence 64, Appl
13	433	20.6	533	6	US-10-449-902-47361 Sequence 47361, A
14	429.5	20.4	538	6	US-10-449-902-44533 Sequence 44533, A
15	428	20.3	459	6	US-10-953-349-906 Sequence 906, App
16	428	20.3	529	6	US-10-953-349-905 Sequence 905, App
17	428	20.3	543	6	US-10-953-349-904 Sequence 904, App
18	427.5	20.3	533	6	US-10-449-902-52316 Sequence 52316, A
19	426	20.2	550	6	US-10-449-902-46303 Sequence 46303, A
20	426	20.2	563	6	US-10-449-902-51194 Sequence 51194, A
21	425	20.2	547	6	US-10-449-902-54833 Sequence 54833, A
22	414.5	19.7	542	6	US-10-449-902-44416 Sequence 44416, A
23	410.5	19.5	551	6	US-10-449-902-33055 Sequence 33055, A
24	404	19.2	527	6	US-10-449-902-44411 Sequence 44411, A
25	402	19.1	508	6	US-10-449-902-47145 Sequence 47145, A

26	397	18.9	608	7	US-11-312-958-4	Sequence 4, Appli
27	397	18.9	655	7	US-11-312-958-36	Sequence 36, Appl
28	391.5	18.6	534	6	US-10-449-902-43354	Sequence 43354, A
29	379.5	18.0	456	6	US-10-449-902-32014	Sequence 32014, A
30	379.5	18.0	456	6	US-10-449-902-32452	Sequence 32452, A
31	379.5	18.0	456	6	US-10-449-902-53780	Sequence 53780, A
32	374.5	17.8	372	6	US-10-953-349-10927	Sequence 10927, A
33	374.5	17.8	431	6	US-10-505-928-845	Sequence 845, App
34	373	17.7	516	6	US-10-449-902-48594	Sequence 48594, A
35	372	17.7	339	6	US-10-449-902-49041	Sequence 49041, A
36	370	17.6	565	6	US-10-449-902-56186	Sequence 56186, A
37	368	17.5	351	6	US-10-505-928-658	Sequence 658, App
38	365	17.3	466	6	US-10-449-902-38177	Sequence 38177, A
39	363	17.2	334	6	US-10-449-902-56570	Sequence 56570, A
40	362.5	17.2	435	6	US-10-953-349-649	Sequence 649, App
41	358	17.0	342	6	US-10-449-902-31553	Sequence 31553, A
42	358	17.0	342	6	US-10-449-902-46910	Sequence 46910, A
43	357.5	17.0	461	6	US-10-449-902-43487	Sequence 43487, A
44	357	17.0	520	6	US-10-449-902-45088	Sequence 45088, A
45	356.5	16.9	461	6	US-10-449-902-49645	Sequence 49645, A

ALIGNMENTS

RESULT 1
US-11-273-567-4
; Sequence 4, Application US/11273567
; Publication No. US20060115453A1
; GENERAL INFORMATION:
; APPLICANT: Yaffe, Michael B.
; APPLICANT: Manke, Isaac A.
; APPLICANT: Reinhardt, Hans Christian
; APPLICANT: Lim, Daniel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING CELLULAR PROLIFERATIVE
; DISEASES
; FILE REFERENCE: 01997/557002
; CURRENT APPLICATION NUMBER: US/11/273,567
; CURRENT FILING DATE: 2005-11-14
; PRIOR APPLICATION NUMBER: 60/627,352
; PRIOR FILING DATE: 2004-11-12
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-273-567-4

Query Match 100.0%; Score 2106; DB 7; Length 400;
Best Local Similarity 100.0%; Pred. No. 3e-96;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	VTSQVLGKLVQIFNKRTQEKFKMLQDCPKARREVELHWRASQC	PHIVRVDVY	120
Db	65	VTSQVLGKLVQIFNKRTQEKFKMLQDCPKARREVELHWRASQC	PHIVRVDVY	124
Qy	121	ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDOAF	TEREASEIMKSIGEAIOYLSINIAH	180
Db	125	ENLYAGRKCLLIIVMECLDGGELFSRIQDRGDOAF	TEREASEIMKSIGEAIOYLSINIAH	184
Qy	181	RDVKPENLLYTSKRPNAILKLTDFGAKET	TSNSLTPCYTPYVAPEVLGPEKYDKSC	240
Db	185	RDVKPENLLYTSKRPNAILKLTDFGAKET	TSNSLTPCYTPYVAPEVLGPEKYDKSC	244
Qy	241	DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEF	FPNPEWSEVSEVKMLIRN	300
Db	245	DMWSLGVIMYILLCGYPFPFYSNHGLAISPGMKTRIRMGQYEF	FPNPEWSEVSEVKMLIRN	304

Db 15 SQSQSPSPHHKHHHQTTRAPKPKPKPPPP--QQPRSQPPPPRHQPPQQAQAAAE 72

QY 46 SGLQIKKNAIIDDYKVT---SQVLGLGINGKVLQIFNKRTOEKFALKML-----QDC 94

Db 73 DGVRVLGRPMEDVRATYTFGRELGRGQFGVTYLATHKPTGRRYACKSTAARKLARPDLL 132

QY 95 PKARREVELHWRASQCPHIVRIVDVYENLYAGRKCLLIIVMECLDGGELFSRIQDRGDQAF 154

Db 133 DDVRRREVHMHHLTGHRIIVELRGAYED----RHSVNLVMELCGEGELFDRIIARGH--Y 186

QY 155 TEREASEIMKSIGEAIQYLHSINIAHRDVKPENLLYTSKRPNAILKLTDFG---FAKETT 211

Db 187 SERAAALCREIVSVVHSHCHSMGMVHRDLKPENFLFLNKRDESPLKATDFGLSVFFKPGE 246

QY 212 SHNSLTTPCYTPYVVAPEVLGPEKYDKSCDMWSLGVIMYILLCGYPPFYSNHGLAISPGM 271

Db 247 QFRDLVG---SAYVVAPEVL-KRLYGAEADIWSAGVILYILLSGVPPFWAEN---EDGI 298

QY 272 KTRIRMGQYEFNPNPEWSEVSEVKMLIRNLLKTEPTQRMTEFNMNHPWIMQSTKVPQTP 331

Db 299 FDAVLQGHIDESSEPWPSISSGAKDLVKRMLRQDPKERLTAAEILNHPWIREDGEAPDKP 358

QY 332 L 332

Db 359 L 359

RESULT 5

US-11-242-505A-42

; Sequence 42, Application US/11242505A

; Publication No. US20060099656A1

; GENERAL INFORMATION:

; APPLICANT: Carroll, Joseph M.

; APPLICANT: Healy, Aileen

; TITLE OF INVENTION: Methods and Compositions for Treating

; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,

; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,

; FILE REFERENCE: MPI2001-288P1RCP1OMNIM

; CURRENT APPLICATION NUMBER: US/11/242,505A

; CURRENT FILING DATE: 2005-10-03

; PRIOR APPLICATION NUMBER: US 10/290,078

; PRIOR FILING DATE: 2002-11-07

; PRIOR APPLICATION NUMBER: US 60/347,949

; PRIOR FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: US 10/320,351

; PRIOR FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: 60/341,606

; PRIOR FILING DATE: 2001-12-17

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 42

; LENGTH: 473

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-242-505A-42

Query Match 23.1%; Score 487.5; DB 7; Length 473;

Best Local Similarity 37.5%; Pred. No. 1.6e-17;

Matches 111; Conservative 55; Mismatches 113; Indels 17; Gaps 7;

QY 29 AQPPPPPPQFPQFHVKSGLQIKKNAIIDDYKVTSQLGLGINGKVLQIFNKRTOEKFAL 88

Db 19 ASAAPGTASLVPDYWIDGS--NRDALSDFFEVESE-LGRGATSIVYRCKQGTQKPYAL 74

QY 89 KMLQ---DCPKARREVELHWRASQCPHIVRIVDVYENLYAGRKCLLIIVMECLDGGELFSR 145

Db 75 KVLKKTVDKKIVRTEIGVLLRLSH-PNIIKLKEIFETPTE----ISLVLELVTGGELFDR 129

QY 146 IQDRGDOAFTEREASEIMKSIGEAIQYLHSINIAHRDVKPENLLYTSKRPNAILKLTDFG 205

Db 130 IVEKG--YYSERDAADAVKQILEAVAYLHENGIVHRDLKPENLLYATPADAPLKIADFG 187

QY 206 FAKETTSNLSLTTPCYTPYVVAPEVLGPEKYDKSCDMWSLGVIMYILLCGYPPFYSNHGL 265

Db 188 LSKIVEHQVLMKTVCGTPGYCAPEILRGCAYPEVDMWSVGIIITYILLCGFEPFYDERG- 246

QY 266 AISPCKMKTIRMGQYEFNPNPEWSEVSEVKMLIRNLLKTEPTQRMTEFNMNHPWI 321

Db 247 --DQFMFRILNCEYYFISPPWDEVSLNAKDLVRKLIIVLDPKKRLTTFQALQHPWV 300

RESULT 6

US-10-449-902-50362

; Sequence 50362, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

; FILE REFERENCE: MOA-A0205Y1-US

; CURRENT APPLICATION NUMBER: US/10/449,902

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: JP 2002-203269

; PRIOR FILING DATE: 2002-05-30

; PRIOR APPLICATION NUMBER: JP 2002-383870

; PRIOR FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 56791

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 50362

; LENGTH: 623

; TYPE: PRT

; ORGANISM: Oryza sativa

US-10-449-902-50362

Query Match 22.9%; Score 483; DB 6; Length 623;

Best Local Similarity 29.6%; Pred. No. 3.3e-17;

Matches 128; Conservative 68; Mismatches 148; Indels 88; Gaps 13;

QY 13 PAPPQPPTPALPHPPAQPPP-----PPPQFP 40

Db 50 PAPP--PPTSDAPLAVQNKPPEHVKIVSTTDTASAEQDASKSSAGSDSGEAPRPRVPP 107

QY 41 QFHVXSG-----LQIKKNAIIDDYKVTSQLGLGINGKVLQIFNKRTOEKFALKML-- 91

Db 108 VKRVSSAGLLVGSVLKRKTESLKDYSL-GRKLGGQFGTTVLCVERATGKEFACKSILK 166

QY 92 -----QDCPKARREVELHWRASQCPHIVRIVDVYENLYAGRKCLLIIVMECLDGGELFSR 145

Db 167 RKLVTDDDEDVREIQIMYHLAGHPNVISIRGAYEDAVA---VHLVMELCAGGELFDR 222

QY 146 IQDRGDOAFTEREASEIMKSIGEAIQYLHSINIAHRDVKPENLLYTSKRPNAILKLTDFG 205

Db 223 IVQKGH--YTERKAAELARVIGVVEVCHSMGMVHRDLKPENFLFADQTEEAALKTIDFG 280

QY 206 FAKETTSNLSLTTPCYTPYVVAPEVLGPEKYDKSCDMWSLGVIMYILLCGYPPFYSNHGL 265

Db 281 LSIFRPGQVFTDVVGSPYYVAPEVL-KKYGQEADVWSAGVIYILLCGVPPFWAEN-- 337

QY 266 AISPCKMKTIRMGQYEFNPNPEWSEVSEVKMLIRNLLKTEPTQRMTEFNMNHPWIMQST 325

Db 338 --EQGIFEEVLHGRDLDFQSEPWPSISEGAKDLVRRMLVRDPKKRLTAHEVLRHPWVQVG 395

QY 326 KVPQTPLHTSRVLKEDKE-----RWEDVKEEMTSALATM-----RV 361

Db 396 LAPDKPL-DSAVLSRMKQFSAMNKKLMALRVIAENLSEDEIAGLKEMFKMIDTDSGQI 454

QY 362 DYEQIKI--KKI 371

Db 455 TFEELKVGLKKV 466

RESULT 7

US-10-505-928-349

; Sequence 349, Application US/10505928

Db 278 YGPE-----VDIWSAGVILYILLCGVPPFWAE-----TEQGVARAILRGAADFREPWPRI 328
QY 291 SEEVKMLIRNLKTEPTQRTMTITEFNMHPWIMQSTKVQPOTPLHTSRVLKEDKERWEDVKE 350
Db 329 SRAAKSLVRQMLDVPRRRPTAQOVLDPHLHHAARAPNVPL--GDVVRARLKQFSLMNR 386
QY 351 EMTSALATMRVDYEQIKIKKIE 372
Db 387 LKKKA--MRVIAEHLVVEEVE 405

RESULT 10
US-11-312-958-34
; Sequence 34, Application US/11312958
; Publication No. US20060100152A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
; TITLE OF INVENTION: 13424 MOLECULES
; FILE REFERENCE: MPI02-027P1RNMOMIN
; CURRENT APPLICATION NUMBER: US/11/312,958
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/10/369,022
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/360,495
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/370,121
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/373,010
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/373,908
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/377,717
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/379,949
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/382,409
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/385,280
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/386,879
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-312-958-34

Query Match 20.7%; Score 435.5; DB 7; Length 766;
Best Local Similarity 32.9%; Pred. No. 8.1e-15;
Matches 114; Conservative 61; Mismatches 134; Indels 37; Gaps 14;
QY 51 KKNALIDDYKVTSQVLGLGINGKVLQIFNKRTQEKFALKMLQD---CPK---ARREVELH 104
Db 386 ESSTLLEKYKI-GKVIQDGNFAVVKECIDRSTGKEFALKIIDKAKCCGKEHLIENEVSIL 444
QY 105 WRASQCPHIVRIVDVYENLYAGRKCLLIIVMECLDGGELFSRIQDRGDAQFTEREASEIMK 164
Db 445 RRVKH-PNIIMLVEEMETATE-----LFLVMELVKGGLDFDAI--TSSTKYTERDGSAMVY 497
QY 165 SIGEAIQYLHSINIAHRDVKPNLLYTSKRPNAI--LKLTDGFGAKETTSNLSLTPCYT 222
Db 498 NLANALRYLHGLSIVHRDIKPENLL-VCEYPDGTGKSLKLGDFGLA--TVVEGPLYTVCGT 554

QY 223 PYYVAPEVLGPEKYDKSCDMWSLGVIMYILLCGYPPFPYSNHGLAISPGMKTRIRMGQYEF 282
Db 555 PTYVAPEIIAETGYGLKVDIWAAGVITYILLCGFPFPRSENNL--QEDLFDQILAGKLEF 612
QY 283 PNPEWSEVSEEVKMLIRNLKTEPTQRTMTITEFNMHPWI-----MQSTKVPQOTPLH 333
Db 613 PAPYWDNITDSAKELISQMLQVNVEARCTAGQILSHPWVSDASQENNMQA EVTGKLKQH 672
QY 334 TSRVLKEDKERWEDVKEEMTSALATMRVDYE-QIKIKK-IEDASNP 377
Db 673 FNNALPKQNSTTTGVSVMINTAL-----DKEGQIFCSKHCQDSGRP 713

RESULT 11
US-10-449-902-46406
; Sequence 46406, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-Oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46406
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-46406

Query Match 20.6%; Score 434; DB 6; Length 568;
Best Local Similarity 27.9%; Pred. No. 7.4e-15;
Matches 122; Conservative 70; Mismatches 156; Indels 90; Gaps 12;
QY 28 PAQPPPPPPQFPQFHVKSGLQIKKNAIID----- 57
Db 35 PSQPPGYPPRESSHSSVTSSTAPERVTIADSDLSSTPNKGNKPKVRRVQSAGLLADSV 94
QY 58 -----DYKVTSQLGLGINGKVLQIFNKRTQEKFALKML-----QDCPKARRE 100
Db 95 LKRDSERLKDLYTLGKLGQGFQGTTCVEKATGKVLACKSIARKKLVS EEDVEDVRRE 154
QY 101 VELHWRASQCPHIVRIVDVYENLYAGRKCLLIIVMECLDGGELFSRIQDRGDAQFTEREAS 160
Db 155 IQIMHHLAGHPSVVSIVGAYEDAVA----VHLVMELCAGGELFDRIVQRGH--YSEKAAA 208
QY 161 EIMKSIGEAIQYLHSINIAHRDVKPNLLYTSKRPNAILKLTDFG---FAKETTSNLSLT 217
Db 209 QLARVIGVVEACHSLGVNHRDLKPNENFLFVNHKEDSPLKTI DFGLSIFFKPGENYSDV 268
QY 218 TPCYTPYYVAPEVLGPEKYDKSCDMWSLGVIMYILLCGYPPFPYSNHGLAISPGMKTRIRM 277
Db 269 G---SPYYVAPEVL-MKHYGREVDVWSAGVIIYILLSGVPPFWDES----EQGIFEKVLK 320
QY 278 QGYEFPNPEWSEVSEEVKMLIRNLKTEPTQRTMTITEFNMHPWIMQSTKVQPOTPLHTS-- 335
Db 321 GDLDFSSDPWPAPISAKDLVRKMLNRDPRKRLTAHEALCHPWVCVDGVAPDKPLD S AVL 380
QY 336 -----RVLKEDKERWEDVK-EEMTSALAT---MRVDYEQIKIKKIEDA 374
Db 381 TRLKQFSAMNKLKMKALRVIAENLSEDEIARLEMPKMLD TDNSGQITLEELKTGLRRVG 440
QY 375 SNPLLLKRRKKARALEAA 392

Db	441	AN----	LKDSEITTLMEAA	455	
US-11-312-958-64					
RESULT 12					
US-11-312-958-64					
; Sequence 64, Application US/11312958					
; Publication No. US20060100152A1					
; GENERAL INFORMATION:					
; APPLICANT: Millennium Pharmaceuticals, Inc.					
; APPLICANT: Rosenfeld, Julie Beth					
; APPLICANT: Silos-Santiago, Inmaculada					
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING					
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,					
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,					
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,					
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR					
; TITLE OF INVENTION: 13424 MOLECULES					
; FILE REFERENCE: MP102-027P1RNMNIM					
; CURRENT APPLICATION NUMBER: US/11/312,958					
; CURRENT FILING DATE: 2005-12-20					
; PRIOR APPLICATION NUMBER: US/10/369,022					
; PRIOR FILING DATE: 2003-02-19					
; PRIOR APPLICATION NUMBER: US 60/360,495					
; PRIOR FILING DATE: 2002-02-28					
; PRIOR APPLICATION NUMBER: US 60/370,121					
; PRIOR FILING DATE: 2002-04-04					
; PRIOR APPLICATION NUMBER: US 60/373,010					
; PRIOR FILING DATE: 2002-04-16					
; PRIOR APPLICATION NUMBER: US 60/373,908					
; PRIOR FILING DATE: 2002-04-19					
; PRIOR APPLICATION NUMBER: US 60/377,717					
; PRIOR FILING DATE: 2002-05-03					
; PRIOR APPLICATION NUMBER: US 60/379,949					
; PRIOR FILING DATE: 2002-05-13					
; PRIOR APPLICATION NUMBER: US 60/382,409					
; PRIOR FILING DATE: 2002-05-21					
; PRIOR APPLICATION NUMBER: US 60/385,280					
; PRIOR FILING DATE: 2002-06-03					
; PRIOR APPLICATION NUMBER: US 60/386,879					
; PRIOR FILING DATE: 2002-06-06					
; Remaining Prior Application data removed - See File Wrapper or PALM.					
; NUMBER OF SEQ ID NOS: 64					
; SOFTWARE: FastSEQ for Windows Version 4.0					
; SEQ ID NO 64					
; LENGTH: 729					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-11-312-958-64					
Query Match					
Best Local Similarity 20.6%; Score 434; DB 7; Length 729;					
Matches 110; Conservative 46; Mismatches 99; Indels 38; Gaps 12;					
QY	45	KSGLOIKKNAIDDDYKVT	SOVLGLGINGKVLQIFNKR	TQEFKALKMLQDCPKAR	----- 98
Db	377	EGGQIPA-TITERYKV	-GRTIGDGNFAVVKEC	VERSTAREYALKIKK-SKCRGKEHMI	433
QY	99	-REVELHWRASQC	PHIVRIV---DVYENLYAGRKCLLI	VMECLDGGELFSRIQDRGDQAF	154
Db	434	QNEVSILRRVKH-PNIV	LLIEEMDVPTELY-----LVMELVKG	GDLFDAL--TSTNKY	483
QY	155	TEREASEIMKSGEAIQ	YLSINIAHRDVKPNLL-YTSKRP	NAILKLTDFGFAKETTSH	213
Db	484	TERDASGMLYNLASA	IKYLSNIVHRDIKPNLLVYEHQ	DGSKSLKLGDFGLA--TIVD	541
QY	214	NSLTPCYTPYVVAPE	VLGPEKYDKSCDMWSLG	VIMYILLCGYPPFYSNHGLAISP	--- 270
Db	542	GPLYTVCGTPTYVAPE	IIAETGYGLKVDIWAAG	VITYILLCGFPFRGS-----GDDQ	594
QY	271	--MKTRIRMGQYEF	NPWSEVSEEVKMLIRNL	LKTEPTQRTMTITEFMNHPWI	321
Db	595	EVbFDQILMGQVDF	SPYWDNVS	DSAKELITMMLLVDDVDQ	RFSAVQVLEHPWV 647

US-10-449-902-47361					
RESULT 13					
US-10-449-902-47361					
; Sequence 47361, Application US/10449902					
; Publication No. US20060123505A1					
; GENERAL INFORMATION:					
; APPLICANT: National Institute of Agrobiological Sciences.					
; APPLICANT: Bio-oriented Technology Research Advancement Institution.					
; APPLICANT: The Institute of Physical and Chemical Research.					
; APPLICANT: Foundation for Advancement of International Science.					
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF					
; FILE REFERENCE: MOA-A0205Y1-US					
; CURRENT APPLICATION NUMBER: US/10/449,902					
; CURRENT FILING DATE: 2003-05-29					
; PRIOR APPLICATION NUMBER: JP 2002-203269					
; PRIOR FILING DATE: 2002-05-30					
; PRIOR APPLICATION NUMBER: JP 2002-383870					
; PRIOR FILING DATE: 2002-12-11					
; NUMBER OF SEQ ID NOS: 56791					
; SOFTWARE: PatentIn Ver. 2.1					
; SEQ ID NO 47361					
; LENGTH: 533					
; TYPE: PRT					
; ORGANISM: Oryza sativa					
US-10-449-902-47361					
Query Match					
Best Local Similarity 20.6%; Score 433; DB 6; Length 533;					
Matches 124; Conservative 68; Mismatches 146; Indels 96; Gaps 16;					
QY	11	PAPAPP----	PQPP-----TPALPHPPA	QPP---PPPPQ-----FPQFHVKSGLQIK	51
Db	29	PAQTTPSYNHPQPP	PPPAEVRYTPSAMNP	VPVPVVPVAPKPTPTDILGKPYDDVRSVYVLG	88
QY	52	KNAIDDDYKVT	SOVLGLGINGKVLQIFNKR	TQEFKALKMLQ-----DCPKARREVEL	103
Db	89	KE-----	LGRGQGVTYLCTE	IASGKQYACKSISKRLVSKADKEDIRREIQI	136
QY	104	HWRASQC	PHIVRIVDVYENLYAGRKCLLI	VMECLDGGELFSRIQDRGDQAFTEREASEIM	163
Db	137	MOHLSGQQN	IVFRGAYED---KSNVHV	VMELCAGGELEFDRIIAKGH--YSERAAATIC	190
QY	164	KSTGEAIQYL	HSINIAHRDVKPNLLYT	SKRPNAILKLTDFG---FAKETTSHNSLTTPC	220
Db	191	RAVVNVVN	ICHFMGMHRDLKPN	FLLATKEENAMLKATDFGLSVFIEEGKMYRDIVG--	248
QY	221	YTPYVVAPE	VLGPEKYDKSCDMWSLG	VIMYILLCGYPPFYSNHGLAISP	GMKTRIRMGQY 280
Db	249	-SAYVVAPE	VL-RRNYGKEIDVMSAG	VILYILLSGVPPFWAB-----TEKGFIDAILQGEI	302
QY	281	EFNPPEWSEV	SEEVKMLIRNLKTEPT	QRTMTITEFMNHPWIMQSTKV	POTPLHTSRVLKE 340
Db	303	DFESQWP	PSISESAKDLVRKMLTQ	DPKKRITSQAVLQHPW-LRDGEASDKPI-DSAVLSR	360
QY	341	DKE-----	-----RWEDVK-----	-----EEMTSALATMRVD	362
Db	361	MKQFRAMN	KLKMKALKVIA	SNLNEEEIKGLKQMF	TNMDTDNSGTITYEELKAGLAKLGSK 420
QY	363	YEQIKIKK	IEDASN 376		
Db	421	LSEAEV	QQLMEAAD 434		
RESULT 14					
US-10-449-902-44533					
; Sequence 44533, Application US/10449902					
; Publication No. US20060123505A1					
; GENERAL INFORMATION:					
; APPLICANT: National Institute of Agrobiological Sciences.					
; APPLICANT: Bio-oriented Technology Research Advancement Institution.					
; APPLICANT: The Institute of Physical and Chemical Research.					
; APPLICANT: Foundation for Advancement of International Science.					
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF					

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